MORPHICH V - 3 RIL 414 ⇒> fil heaplus FILE 'HOAFLYS' ENTERED AT 13:80:24 CN 13 FEB 2003 USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT. PLEASE SEE "HELF USAGETERMS" FOR DETAILS. COPYRIGHT (6) 1/03 AMERICAN CHEMICAL SOCIETY (ACS) Copyright of the articles to which records in this actabase refer is held by the publishers listed in the PUBLISHER (FB, field (available for records published or updated in Chemical Abstracts after December 25, 1996), unless otherwise indicated in the original publications. The CA Lexison is the copyrighted intellectual property of the the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or styring of this information, without the prior written insent of "Wa", is strictly prohibit-i. FILE COVERS 1907 - 13 Feb 2003 - VOL 138 TGS " FILE LAST UPDATED: 12 Feb 2003 (20030212/ED) This file contains CAS Redistry Numbers for easy and accurate substance identification. = . = · $= \cdot$ d stat que 17 1 SEA FILE=REGISTRY ABB=ON PLU=ON WVRWHF/SQSP Γ : 38 SEA FILE=REGISTRY ABB=ON PLU=ON W[GAILVSTR][GAILVSTR]WHF/SQSP 1 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 27 SEA FILE=HCAPLUS ABB=ON FILE=N L3 1 SEA FILE=HCAPLUS ABB=ON FILE=N L3 L۶ L^{\perp} L 11/ AND 18 = d ibib abs hitrn 17 1 AMSWER 1 DF 1 HCAPLUS COPYRIGHT 2003 A08 ESSION NUMBER: 2000:535163 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: TITLE: 133:145915 Transcription factor E2F DNA-binding domain inhibitor peptides and uses thereof Muller, Rolf; Kontermann, Roland Ernst; Montigiani, INVENTOR(S): Silvia Prolifix Limited, UK PATENT ASSIGNEE(S): PCT Int. Appl., 42 pp. SOURCE: MODEN: FIRMIN DOCUMENT TYPE: Fatent LANGUAGE: English FAMILY ACC. NUM. COUNT: PATENT INFORMATION:

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RW: GH, GM, KE, LS, MW, SD, SL, DD, TZ, DG, EW, AT, BE, DH, DY, LE, DK, ES, FI, FR, GB, GP, IE, II, LU, MD, ML, ET, SE, BF, HJ, DF, CG, TI, CM, GA, SN, JW, ML, ME, ME, SN, TD, TG
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GB 1999-1710 A 19990126
WO 2009-GB227 W 20000126
 PRIORITY APPLN. INFO.:
                                                                                 WO 2000-GB227
                                       MARPAT 133:145915
OTHER SOURCE(S):
          The present invention provides sequences of peptides which bind to the DNA
          binding domain of transcription factor E2F, and inhibit cell cycle
          progression. Peptides include FWLRFT, WVRWHF, WHFIFW, IWLSGLSRGVWVSFP,
          and GSRILTFRSGSWYAS and derivs. based upon these sequences. Compns. and
          the use or the peptides in inhibiting sell syste progression, such as in
          uncontrolled sell proliferation, are also provided.
          286839-16-5P
          RL: BAC (Biological activity or effector, except adverse); BOC (Biological
          occurrence); BSU (Biological study, unclassified); BUU (Biological use,
          unclassified); PRF (Properties); SPM (Synthetic preparation); BIOL
           (Biological study); 0000 (Goourrence); PREF (Preparation); (SES (Usas
                *peptide sequence; transcription factor ELF DNA-binding achain
                inhibitor peptides and uses thereof
          286839-22-3 286839-23-4
          RL: PRF (Properties)
                +unclaimed sequence; transcription factor E2F DNA-binding domain
                inhibitor peptides and uses thereof)
REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS
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Crossover limits have been increased. See HELF CROSSOVER for details.
Emperimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STMote 27, Searching Properties
in the CAS Registry File, for complete details:
http://www.cas.org/CNLINE/STN/STNOTES stnotesio.pdf
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LII ANSWER 1 OF 26 HOAPLUS COPYRIGHT 2503 ACS
ACCESSION NUMBER:
                            2002:850304 HCAPLUS
DOCUMENT NUMBER:
                              137:347570
TITLE:
                              Cloning and cDNA and deduced amino acid sequences of
                              69 human proteins and their diagnostic and therapeutic
                              uses
INVENTOR (S):
                               Ruben, Steven M.; Parash, Steven M.; Bosch, Stald A.;
                              Birse, Charles A.
Human Genome Sciences, Inc., USA
PATENT ASSIGNEE(S):
SOURCE:
                               U.S. Pat. Appl. Publ., 194 pp., Cont.-in-part of Appl.
                              No. PCT/US01/01346.
                              CODEN: USMKCO
DOCUMENT TYPE:
                              Patent
LANGUAGE:
                              English
FAMILY ACC. NUM. COUNT:
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US 2000-236327P P 20000929
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US 2000-0818568 P 20001208
US 2000-251866P P 20001208
US 2000-251869P P 20001208
US 2001-764863 B1 20010117
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AB The present invention relates to 59 novel human proteins and isolated nucleic acids contg. the coding regions of the genes encoding such proteins. Tissue distribution, sequence nomelogies, and preferred epitope sites are provided for the proteins, as well as chromosomal mapping of some of the denes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human proteins. High-throughput screening assays are also provided for various putative activities of the proteins.

474183-38-5P, Protein (human clone HFIEC13) TT FL: BFN (Biosynthetic preparation ; BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); TAU (Therapeutic use); BIOL

(Biological study); PREP (Preparation); USES (Uses)

(amino acid sequence; cloning and cDNA and deduced amino acid sequences of 69 numan proteins and their diagnostic and therapeutic uses)

L11 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2003 ACS ADDESSION NUMBER: 2002:723249 HCAPLUS

DOCUMENT NUMBER:

137:227411

TITLE:

Whole-genome comparison of Mycobasterium tubersulosis

clinical and laboratory strains

AUTHOR(S):

Fleischmann, R. D.; Alland, D.; Eisen, J. A.; Carpenter, L.; White, O.; Peterson, J.; DeBoy, R.; Dodson, F.; Gwinn, M.; Haft, D.; Hickey, E.; Kolonay,

J. F.; Nelson, W. C.; Umayam, L. A.; Ermolaeva, M.; Salzherg, S. L.; Delcher, A.; Utterback, T.; Weidman, J.; Fhouri, H.; Gill, J.; Mikula, A.; Bishai, W.;

Jacobs, W. R., Jr.; Venter, J. C.; Fraser, C. M. The Institute for Genomic Research, Rockville, MD,

SOURCE:

CORPORATE SOURCE:

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Coopen: Jobany, ISSN: //Li-9193 American Society for Microbiology

PUBLISHER: DOCUMENT TYPE: Cournal

LANGUAGE: English

AB Virulence and immunity are poorly understood in Mycobacterium tuberculosis. The complete genome of the M. tuberculosis clin. strain CDC1551 was sequences and a whole-genome comparison with the lab. strain HPTRy performed in order to identify polynorphic sequences with potential relevance to disease pathogenesis, immunity, and evolution. Large-sequence and single-nuclectide polymorphisms were found in numerous genes. Folymorphic losi included a phospholipase C, a membrane lipoprotein, members of an adenylate cyclase gene family, and members of the FE'FFE gene family, some of which have been implicated in virulence or the host immune response. Several gene families, including the FE/FFE gene family, also had significantly higher synonymous and nonsynonymous

substitution trequencies compared to the genome as a whole. A large sample of M. tuberculosis clim. isolates was tested for a subset of the large-sequence and single-nucleotide polymorphisms and widespread genetic variability was found at many of these loci. Phylogenetic and epidemiol. anal. was barried out to investigate the evolutionary relationships among isolates and the origins of specific polymorphic loci. A no. of these polymorphisms appear to have obsurred multiple times as independent events, suggesting that these changes may be under selective pressure. Together, these results demonstrate that polymorphisms among M. tuberculosis strains are more extensive than initially anticipated, and genetic variation may have an important role in disease pathogenesis and immunity. The sequence of the clin. strain CDC1881 of M. tuberculosis was deposited in GenBank/EMBL/DDBJ under accession no. AE000516, and the sequence of the genome of the M. tuberrulisis lab. strain H37kv was recently sequenced and deposited as N. 90.362.

457684-48-9

RL: BSU (Biological study, unclassions), AFF (Frigerick), Fill (Biological study)

(amino acid sequence; whole-denome commanison of Mycobacterium tuberculosis clin. and lab. strains

REFERENCE COUNT:

THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS = = RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 26 HCAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:545718 HOAPLUS

DOCUMENT NUMBER:

137:74287

TITLE:

SOURCE:

PUBLISHER:

The genome of Methanosarcina mazei: evidence for lateral gene transfer between bacteria and Archaea

AUTHOR(S):Deppenmeier, Uwe; Johann, Andre; Hartsch, Thomas; Merkl, Rainer; Schmitz, Ruth A.; Martinez-Arias, Rosa;

Henne, Anke; Wiezer, Arnim; Baumer, Sebastian; Jacobi, Carsten; Bruggemann, Holger; Lienard, Tanja;

Christmann, Andreas; Pomeke, Mechthild; Steckel, Silke; Bhattacharyya, Anamitra; Lykidis, Athanasios; Overbeek, Ross; Klenk, Hans-Feter; Gunsalus, Robert

F.; Fritz, Hans-Joachim; Gottschalk, Gerhard

CORPORATE SOURCE: Gottingen Genomics Laboratory. Department of General

Microbiology. Institute of Microbiology and Genetics, Georg-August-Thiversity, Goethingen, 2-37007, Germany Journal of Molegular Microbiology and Biotechnology

(2002), 4(4), 453-461

Horizon Scientific Fress

DOCUMENT TYPE: Journal

LANGUAGE: English

The Archaeon Methanosarcina mazei and related species are of great ecol. importance as they are the only organisms fermenting acetate, methylamines and methanol to methane, carbon dioxide and ammonia (in case of methylamines). Since acetate is the precursor of 60 of the methane produced on earth these organisms contribute significantly to the prodn. of this greenhouse gas, e.g. in rice paddies. The $4,196,340\ \mathrm{base\ pairs}$ circular chromosome of M. mapel is more than twice as large as the genomes of the methanogenic Archaea currently completely sequenced. There were 3371 open reading frames (ORFs) identified. Based on currently available sequence data 376 of these ORFs are Methanosardina-specific and 1043 ORFs sequence data from or these ORPs are Methanosardina-specific and 1343 ORPs find their closest homolog in the bacterial domain. About 644 of these ORPs reach significant similarity values only in the bacterial ideals. They include 16 of the Loo transpolases, and protected involved to cluster the loo transpolases, and protected in 10 map and environmental sensing, general relation, and stream to prince. Of the examples are the observable of the bacterial Brofil Brofil map in system and the presence of tetrahydroclass are the presence of tetrahydroclasses. These timings might indicate that lateral gene transfer has played an important

evolutionary role in forming the physical of this metabolically wereatile methanogen. The genome sequence is deposited in JenBank under Attession No. AEQĴ83%4.

440301-84-8

RL: BSU Biological study, unclassified; FBP Frigerties; HEDE Biological study:

quantino avid sequence; complete denome sequence or Methanisar cina maper and evidence for lateral gene transfer between busheria and Armusea

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L11 AMSWER 4 OF 26 HCAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:348600 HCAPLUS

137:25963

Human genome derived single exon nucleic acid probes

useful for gene empression analysis

Penn, Sharron Gaynor; Rank, David Russell; Chen, INVENTOR(S):

Wenshen: Hanzel, David Kagen

FATENT ASSIGNEE, S.: USA

U.S. Fat. Appl. Fubl., 97 pp., Cont.-in-part of U.S. Ser. No. 774,203. SOURCE:

CODEN: USXXCO

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 84

PATENT INFORMATION:

PATENT NO.	MINI CATH		erill verill i	
US 2002048763 GB 2360284 GB 2360284	A1 20020 A1 20010 B2 20020)425	JS 2001-864761 GB 2000-24263	20010523
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US 2002081590 No 2001051210	A1 20020 A3 20010	1809 7	JS 2001-774203 KO 2001-US681	28/12/12/20
CR, CU, HU, ID,	CZ, DE, DH, IL, IN, IS, MA, MD, MG, SG, SI, SH, ZW, AM, AZ, KE, LS, MW,	DM, DZ, EE, JP, KE, KG, MK, MN, MW, SL, TJ, TM, BY, KG, KZ, MZ, SD, SL,	ES, FI, GB, C KP, KR, KZ, I MX, MZ, NO, N TR, TT, TZ, U MD, RU, TJ, T SZ, TZ, UG, 2	SY, BZ, CA, CH, CN, SD, GE, GH, GM, HR, LC, LK, LR, LS, LT, IZ, PL, PT, RO, RU, IA, UG, US, UZ, VN, IM SW, AT, BE, CH, CY,
DE, DK, BJ, OF, WO 2301051271	ES, FI, FF, CS, CI, CD., A2 20010	3A, 21, 11,		II, PT, SE, TR, BF, II, II, TG
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   WO 2001057275
                W: AE, AG, AL, AM, AT, AU, AZ, BA, BE, BG, BR, BY, BZ, CA, CH, CN,
                              CR, CU, CZ, DE, DE, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HE, BU, DD, IL, IN, L', JP, KE, KG, KE, KR, KZ, LC, LK, LE, LS, LT, LU, L', MA, MD, MH, MH, MN, MW, MK, MZ, NO, NZ, PL, PT, RO, RU,
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DE, DK, EG, EI, ER, GB, GR, IE, IT, LU, MG, ML, ET, SE, TR, BE,
PRIORITY APPLN. INFO.:
                                   US 2000-236359P P 20000927
                                   GB 2000+24263 A 20001004
                                  US 2001-774203 A2 20010129
                                  WO 2001-US661 A2 20010130
                                  WO 2001-US662
                                                A2 20010130
                                  NO 2001-US663
                                                A2 20010130
                                                A2 2001718
                                  WO 2001-US665 A2 20010130
                                                A2 2001013
                                  W0 2001-US666
                                                A2 20010130
                                  WO 2001-US667
                                   MO 2001-08668
                                               A2 20010130
                                   WO 2001-US669 A2 20010180
                                  WO 2001-08670 A2 20010130
                                   TS 2001-266960P P 20010208
AR
    Methods and app. for predicting, contirming and displaying functional
    regions from genomic sequence data are used to identify 16,834 unique
    particularly gene expression anal. by microarray. Also presented are
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human genome-derived single exon probes useful for gene expression anal., geneme-derived single exon microarrays that include such probes, peptides encoded by the exons, and antibodies thereto. The human genome-derived single-exch probes are known to be expressed in one or more human tissues or cell types, particularly human brain, neart, liver, fetal liver, placenta, lung, bone marrow, BT474 and other human mammary epithelial cells, Hela and other human cervical epithelial cells, and HBL 100 and other human mammary epithelial cells. The invention provides a method of financing, selling and/or licensing genome-derived single-exon microarrays to sustomer desiring to measure gene expression, comprising: making available for computerized query or subscription service a database having a record corresponding to each genome-derived single exch microarray available for sale and or libense. [This abstr. become is one of ten records for this document necessitated by the large no. I index entries required to tally index the a locational publication of constraints.).

IT 437115-91-8

RL: BSU (Biological study, unclassified); PRF (Proporties); BIOL (Biological study)

[amino acid sequence; human genome derived single exch nucleic acid probes useful for gene expression anal.]

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LII AMSWER 5 OF 06 HOAFLUS COFFRICHT 2003 ACS

ACCEPTION NUMBER: D. 10:08305 HOAFLUC

DOTMENT NUMBER: 1:0:03305 HOAFLUC

TITLE: complete genome sequence of Methanosarcina acetivorans

CLA reveals extensive metabolic and physiological

diversity
```

ATTER BUT :

Balayan, Janes B.; Mussaur, Thay, Boy, Alley; Endricci, Matthew J.; Matthnalu, Bendemter; FitzHugh, Will; Calvo, Sarah; Engels, Reinhard; Smirnov, Serge; Athoor, Deven; Brown, Adam; Allen, Nicele; Naylor, Jerome; Stange-Thomann, Nicole; DeArellanc, Kurt; Johnson, Robin; Linton, Lauren; McEwan, Paul; McKernan, Kevin; Talamas, Jessica; Tirrell, Andrea; Ye, Wenjuan; Zimmer, Andrew; Barber, Robert D.; Cann., Isaac; Graham, David E.; Grahame, David A.; Guss, Adam M.; Hedderich, Feiner; Ingram-Smith, Cheryl; Kueitner, H. Craig; Kroyoki, Joseph A.; Leigh, John A.; Li, Weiwi; Liu, Jinfeng; Mukhopadhyay, Biswarup; Reeve, John M.; Smith, Kerry; Springer, Timothy A.; Umayam, Lowell A.; White, Owen; White, Robert H.; de Macario, Everly Conway; Ferry, James G.; Jarrell, Ker. F.; Jing, Hua; Macario, Alberto J. L.; Faulsen, Tan; Pritchett, Matthew; Cowers, Kevin B.; Swansen, Benaud M.; Minder, Steven H.; Dander, Erry, Methali, Milliam H.; Pirren, 14 Y G 25-

CORPORATE SOURCE:

Whitehead Institute Penter for Bearme Besearth,

Cambridge, MA, CC141, USA

Genome Research (2002), 12(4), 532-542

CODEN: GEREFS; ISSN: 1088-9051 Cold Spring Harbor Laboratory Press

Journal English

SOURCE:

PUBLISHER: DOCUMENT TYPE: LANGUAGE:

AB Methanogenesis, the biol. prodn. of methane, plays a pivotal role in the global carbon bysle and contributes significantly to global warming. The majority of methane in nature is derived from acetate. The complete genome sequence of an acetate-utilizing methanogen, Methanosarcina acetivorans C2A, is now reported. Methanosarcineae are the most metabolically diverse methanogens, thrive in a broad range of environments, and are unique among the Archaea in forming complex multicellular structures. This diversity is reflected in the genome of M. acetivorans. At 5,751,492 base pairs it is by far the largest known archaeul genome. The 4724 open heading trames do be for a strikingly wide and unanticipated variety of metabolic and cellular capabilities. The presence of novel methyltransferases indicates the likelihood or undiscovered natural energy sources for methanogenesis, whereas the presence of single-subunit carbon monoxide dehydrogenases raises the possibility of nonmethanogenic growth. Although motility has not been obsd. in any Methanosarcineae, a flagellin gene cluster and two complete chemotaxis gene clusters were identified. The availability of genetic methods, coupled with its physical and metabolic diversity, makes M. acetivorans a powerful model organism for the study of archaeal biol. genome sequence is deposited in GenBank under Accession No. AE010656-AE011189.

406874-66-6

RL: BSU (Biological study, unclassified); FRP (Properties); BIOL (Piplogical study)

(amino acid sequence; complete genome sequence of Methanosardina acetivorans CRA reveals extensive metabolic and physiol. diversity)
FOUNT: FRE ARE SECITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT BEFFERING ACCE.

LII ANSWER 6 OF 26 HOAFLUS COPYRIGHT 2003 ACM ACCESSION NUMBER: DOCUMENT NUMBER: 2002:280980 HOAFLUS

137:15544

TITLE: Functional annotation of a full-length Analysmanis

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Wekin, Moto akur Murusuka, Murus Maruya, Adad rollini ka, unkor Watou, Marusuka, Waka unko ka Mara Marusuka, Marusuk ATTHER C: Mark ; Endu, Amie ; Amryama, Fendi; Joh , Tour ;

McKelvey 13 Blz414

Muramatsu, Masami; Hayashizaki, Yoshihide; Kawai, Jun; Carninci, Fiero; Itoh, Masayoshi; Ishii, Yoshiyuki; Arakawa, Takasiro; Shibata, Mazuhiro; Chinagawa, Akira; Shinopaki, Batub Flant Mutatic: Employetion Team, Flant Functional DORFIRATE SITERE: Senomics First Stoup, FIREN Jenomin Zoirn ws Center 380 , telel Styadai, Isunuma, 5 Ee 174, Japan Science Washington, 17, United States, 2014 , SOURCE: Dec (Seet), 141-148 Coden: Cottady, 1301: 1, 7, --American Association for the Advancement of Clience PUBLISHER: SCORENT TEFE: Juneau 1 English AB Full-length cDMAs are essential for the correct annotation of genemic sequences and for the functional anal. of genes and their products. About 188,144 RIKEN Arabidopsis full-length (RAFL) cDNA clones were isolated. The 3'-end expressed sequence tags (ESTs) of 155,144 RAFL cDNAs were clustered into 14,668 nonredundant cDNA groups, about 60 of predicted denes. E'-ESTs were also obtained from 14,034 nonredundant cDNA groups and a promoter database constructed. The sequence database of the RAFL CONAs is useful for promoter anal, and correct annotation of predicted transcription units and gene products. Furthermore, the full-length cDNAs are useful resources for analyses of the expression profiles, functions, and structures of plant proteins. [This abstr. record is one of sixteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints. ... IΤ 437141-30-5 RL: BSU (Biological study, unclassified); PBP Properties ; BT L 野食为100mm10mm10mm10mm (amino acid sequence; functional annotation of a full-congrue Arabidopsis cliA collection) 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS REFERENCE COUNT: RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT LII ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:173767
DOCUMENT NUMBER: 136:351357 Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult liver Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; INVENTOR(S): Rank, David E. Molecular Dynamics, Inc., USA PATENT ASSIGNEE(S): PCT Int. Appl., 659 pp. SOURCE: CODEN: FINANTI DOCUMENT TYPE: Fatent LANGUAGE: English FAMILY ACC. NUM. COUNT: 84 PATENT INFORMATION: PATENTING. KIND DATE AFFICIATION NO. DATE

MO 0001067273 AO 00010604 WO 2001-MERSA A0011136 D001057273 A0 00010509 W0 / TI-MB864 A0710180
W: AE, AB, AL, AM, AT, AT, AD, BA, BB, BB, BB, BY, BD, CA, CM, CM, CB, CT, CD, CD, CK, CM, CD, EE, EB, BI, GB, GC, GE, GE, GM, BR, BT, ID, II, IM, IS, CD, KE, KG, KE, KK, KC, LC, LK, LR, LS, LT, LD, LU, MA, MD, MS, MK, MM, MM, MX, MZ, NO, NZ, FL, BT, RO, RU, SD, SE, SS, SI, SK, SL, TC, TM, TB, TT, TZ, CA, CG, US, CZ, VN, YC, CA, CM, AM, AD, BY, KG, KE, MD, RU, TC, TM

EM: GH, GM, KE, LS, MW, MC, SD, SL, SD, TD, UG, ZW, AI, BE, CH, CY, CE, CK, ES, FI, FR, GF, GR, IE, IT, LC, MC, ML, FT, SE, TR, BF, BJ, CF, CB, CI, CM, GA, CM, SW, ML, ME, NE, SN, TD, TG

CS6 LS4 AI 2001 FIT SP A1263 LOTELOGE

GB 2356 284

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UB US6:1294 B1
GB 0361298 A1
GB 0361238 B2
Wh 0100087273 A0
                               20120306
20120306
                                               9B 2101-15291
                                                                 20001004
                                               WO 2001-US864
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              CR, CU, CD, CE, DK, LM, DD, EE, ES, F1, GB, GD, GE, GH, GM, HR, HU, LD, LL, LM, LS, KE, KS, KF, KE, LC, LK, LK, LS, LT, LV, MA, MD, MS, MK, MU, MM, MM, MC, MC, MC, P1, F1, F3, RU,
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          RW: GH, GM, ES, F1, FR, GB, GR, IE, IT, LU, MC, UL, FT, SE, TR, BF,
             PRIORITY APPLN. INFO.:
                                            GB 2000-24263 A 20001004
WO 2001-US664 A 20010130
    A single exon nucleic acid microarray comprising 13,109 single exon
     nucleic acid probes for measuring gene expression in a sample derived from human adult liver is described. These unique exons are within longer
     probe sequences; sequencing confirms the exact chem. structure of each
     probe. Some amplicons have more than one exon, and some exons are
     contained in more than one amplicon. Expression, homol., and functional
     information are provided for the genome-derived single exon probes that
     are expressed significantly in human adult liver cells. Also described
     are 12,886 single exon nucleic acid probes and 12,583 proteins expressed
     in the adult liver and their use in methods for detecting gene empression.
     The genome-derived single exam nubleic abids comprise a novel type of
     nucleic acid microarray for verifying were expression. In arm., workers
     are provided for identitying emonfolous a wasarp to them to , and for
     assigning exens to a single bene.
IT
     420924-39-6
     RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRF (Properties); AMST (Analytical study); BIOL
      (Biological study); USES (Uses)
         (amino acid sequence; human genome-derived single exon nucleic acid
         probes useful for anal. of gene expression in human adult liver)
L11 ANSWER & OF 26 HOAFLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:187777 HOAFLUS
DOCUMENT NUMBER:
                            136:195341
TITLE:
                            Cloning and cDNA and deduced amino acid sequences of
                            21 human secreted proteins
INVENTOR(S):
                           Rosen, Craig A.; Komatsoulis, George A.; Baker, Kevin
                           P.; Birse, Charles E.; Soppet, Caniel B.; Olsen,
                           Henrik S.; Moore, Faul A., Wei, Fing, Fbner, Seinhard;
                            Duan, I. Bowanne; Chi, Yandau; Chil, St. H.; Bis wills,
                           Michèle; Mi, Jian
PATENT ASSIGNEE(S):
                          - Human Geneme Sciences, Inc., USA
SOURCE:
                          FOT Int. Appl., 184 pp.
                           COCCEN: FINANC
COCUMENT TYPE:
                          Fatent
LANGUAGE:
                           En ilish
FAMILY ACC. NUM. COUNT:
     IRIENT N.
                      KIM TATE
                                              AIPLICATION IN . DATE
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           II 2016990 — AI — 21020029 — — WOLT 1-MM1490 — LO 1 11M
WE AE, AR, AI, AM, AT, AM, AM, BA, BR, BR, BR, BM, BM, BM,
     PRIORITY APPLIES.:
AΒ
      such proteins. Tissue distribution, sequence homologies, and preferred
      epitope sites are provided for the secreted proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host
      cells, antibodies, and recombinant methods for producing human secreted
      proteins in hard-rial, insect, and mammalian sells. The intention further relates to diagnostic and therapeutic methods useru. For diagnosing and
      treating disorders related to these hovel human secreted profesins.
      High-throughput screening assays are also provided for various putative
      activities of the secreted proteins.
      400696-91-5P
      RL: BFN (Biosynthetic preparation); BST 'Biological study, unclassified); FRP (Properties); THU (Therapeutic use); BIOL (Biological study); PMEP
      .Preparation); USES (Uses)
         (amino acid seguence; cloning and cLNA and deduced amino acid seguences
         of 21 human secreted proteins)
REFERENCE COUNT:
                             1
                                   THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS
                                     RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L11 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                             2002:125123 HCAPLUS
DOGUNERT NUMBER:
                              130:145954
                              Genome sequence of the plant pathogen Ralstonia
                             solana searum
AUTHOR(S):
                             Salanoubat, M.; Genin, S.; Artiquenave, F.; Gouzy, J.;
                             Mangenot, S.; Ariat, M.; Billault, A.; Brottier, P.;
                             Camus, J. C.; Cattolico, L.; Chandler, M.; Choisne, N.; Claudel-Renard, C.; Cunnac, S.; Demange, N.;
                              Gaspin, C.; Lavie, M.; Moisan, A.; Robert, C.; Saurin,
                              M.; Schiew, T.; Siguier, B.; Thebault, F.; Whalen, M.;
                             Mincker, F., Lerry, M., Weitzennadi, C., F. Ldea, C. Ren engles and MESS TIBES of Edity, the J. Bit. Mature Linari, United English (J.) 2., 411,4871,497-802
CORFURATE SUTRICE:
SOURCE:
                             CODEN: NATUAS; ISSN: 0029-0936
FUBLISHER:
                             Mature Publishing Group
DOCUMENT TYPE:
                             Journal
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LANGUAGE: English

AB Ralstonia sclanacearum is a devastating, scil-borne plant pathogen with a slobal distribution and an unusually wide host range. It is a model system to the ilescation of mole deverminants governing pathogenisity. The complete genome sequence and its anal. of strain GMI1000 is presented. The 8.8-megabase (Mb) genome is organized into two replicons: a 3.7-Mb chromosome and a 2.1-Mb megaplasmid. Both replicons have a mosaic structure providing evidence for the acquisition of genes through horizontal gene transfer. Regions contg. genetically mobile elements assocd, with the percentage of 3.0 bias may have an important function in genome evolution. The senome entoles many proteins potentially assocd, with a role in pathogenisity. In particular, many potential or attachment

Mb891vey 18_911414

lactors were identified. The complete repertoire of type III secreted effector proteins can be studied. Over 40 candidates were identified. Comparison with other genomes suggests that bacterial plant pathogens and aminal pathorens hurbor distinct arrays of specialized type III-dependent

394342-70-2 394342-96-2

RL: BSU (Biological study, unclassified ; PRF (Properties); HIGH Biological study

(amino acid sequence; genome sequence of the plant pathogen Ralstonia solanacearum;

REFERENCE COUNT:

THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RESERVENCES

LII ANGMER I. FILO BIMELITO DIFFERENCI - ANI ATTROCTULI NUMBER: 21 2:11 - 24 ENACION DOCUMENT NUMBER: 13%:227873

Human genome-derived single emon nucleic acid probes useful for analysis of gene expression in human

placenta

INVENTOR (3):

Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;

PATENT ASSIGNEE(S):

Rank, David R. Molecular Dynamics, Inc., USA

FCT Int. Appl., 654 pp.

SOTROE:

conem: FIXND2

DOCUMENT TYPE:

Patent English

LANGUAGE: FAMILY ACC. NUM. COUNT: 84

PATENT INFORMATION:

PATENT NO.	KIMD DATE	AFFLICATION NO. DATE
WO 2001057272		WC 20:1-WPev6 AC 1:1:0
CR, CU,	AL, AM, AT, AC, CZ, DE, DK, DM,	AZ, BA, FB, BG, BR, FY, BC, MA, MH, CN, DZ, BE, FI, GB, GD, GE, GB, GM, HR, HD,
*** ****	1177 1470 x 121 3 147	KG, KB, KR, KE, LC, LK, LR, LS, LT, LC, MW, MM, MM, MM, MD, MD, MD, BL, ET, RD, RD, RD,
SE, SG,	SI, SK, SL, TJ,	TM, TR, TT, TZ, UA, UG, US, UC, VN, YU,
ZA, ZW, RW: GH, GM,		KZ, MD, BC, TC, TM SO, SI, SZ, TZ, TG, CW, AT, BE, CE, CY,
DE, DK,	EC, FI, FR, 3B,	GE, IE, IT, LU, MO, NL, PT, SE, TR, BE,
	CG, CI, CM, GA,	GN, GW, ML, MR, ME, SN, TD, TG
GB 2360284 GB 2360284	A1 20010919 B2 20020227	GB 2000-24263 20001004
GB 2361238	A1 20011017	GB 2001-15281 20001004
GB 2361236 WO 2001050202	B2 20720306	No. 0004 Hacco
WO 2001057272 WO 2001087272	A2 20010809 A3 20030103	WO 2001-US663 20010130
X: AE, AS,	AL, AM, AT, AT,	AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
O.K., O.,		DI, EE, ES, FI, GB, GD, GE, GH, GM, HR, KE, KG, KF, KR, KD, LC, LK, LR, LS, LT,
	MA, MD, MG, MK,	ME, AG, AF, AR, AL, LC, LA, LR, LS, LI, MM, MW, MX, MZ, MO, ME, FL, FT, RO, RU,
SD, SE,	SG, SI, SK, SL,	TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN.
YU, LA, RW: GH, GM,	CH, AH, AC, BY, RR 18 MW MO	KS, KU, MD, RO, TO, TM SD, SL, SO, TZ, OA, OW, AT, BH, MH, CY,
DE, DK,	EO, FI, FF, 3P,	38, IF, IT, III, MY, MI, IT, IF, IB, BE,

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		718 1017] = 618478 A 21071631
		TS 1000-608408 A 20000631 TS 0000-680866 A 20000803 TS 0000-2846878 E 20000801
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iB L H1416+ A Li i i4 WO AllI-tak63 A 20010130 A single exon nujleig acia mi mpiannay hoppisina 19,131 single jesqu nucleic acid probes for measurin; dene empression in a sample derived from human placents cells is described. These unique exche are within longer probe sequences, so per tire whiling the exact then we have a_{ij} pride. Sime aplicing have blue than the emin, and other emin, are contained in mole than one amplicant hapreselts, number, and right in al information are provided for the genome-derived single exon probes that are expressed significantly in human placenta. Also described are 13,000 single exch nucleic acid probes and 12,600 proteins expressed in the planenta cells and their use in methods for detecting gene empression. The genome-derived single ewon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying emons in a eukaryotic genome, and for assigning exchs to a single gene. (This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the accument and publication system constraints.].

400664-75-7

EL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)

(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene empression in human placenta

L11 ANSWER 11 OF LK HOAFLYD MOFYRIGHT L ACCESSION NUMBER: 2002:1106 6 HOAFLYM

DOCUMENT NUMBER: 138:198288

TITLE: Human genome-derived single exon nucleic acid probes

useful for analysis of gene empression in human fetal

liver

INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;

Rank, David R.

PATENT ASSIGNEE S): Molecular Dynamics, Inc., USA

SOURCE: FOT Int. Appl., 639 pp.

CODEN: PINKD2

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 84

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE
WO 2001087277 A2 20010874 WM 2 1-MF/FF 2 201114 W: AE, AG, AL, AM, AT, AU, AD, BA, BB, BG, BR, BY, PE, CA, - 11, - 11, LI, MA, MD, MS, MK, MU, MW, MM, MD, NO, MD, FL, FT, RG, RD, SD, SE, SG, SI, SK, SL, TD, TM, TR, TT, TZ, UA, UG, US, UG, UM, YU, DA, ZW, AM, AD, BY, KG, KD, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MD, SC, SL, SC, TD, TG, DW, AT, BE, CH, DY, DE, LR, EG, FI, FR, BE, GK, IE, IT, LC, MC, ML, FT, SE, TR, BE, GB 2862184

AL 20010919

GB 2861284

AL 20010910

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AL 20010900

MO 2001-18668

AL 20010900

MO 2001090200

MO 2001090200

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BM: GH, EM, EE, LO, MW, ME, SI, DI, DD, DD, DD, DM, AD, EE, MH, MY, DE, DE, DE, ED, EE, EE, GE, DE, DE, DT, MO, MI, ET, SE, TE, EE, EU, OF, OG, CI, SM, SA, GM, MM, ME, ME, SM, TD, TO COMPANY AND ADDRESS AND ADDRESS ADDRESS
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US 2001-827998 20010406

US 2000-180312F F 20000204

US 2000-608408 A 20000630
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TS 10.0-632366 A 2000.863
TS 10.0-2346878 F 20.00.921
TS 2000-2363788 F 20.00.921
TS 2000-2363788 F 20.00.920
                                                                                           HB 201 3-0426 *
W 4 0 0111-7846 *
State 4 4 4
          A single exon nucleic acid mirriarray comprising Lu, the single exon
           nucleic acid probes for measuring gene empression in a sample derived from
            human fetal liver cells is described. These unique excus are within
            longer probe sequences; sequencing contirms the exact chem. Structure of each probe. Some amplicons have more than one exon, and some exons are
            contained in more than one amplicant. Expression, howell, and functional
            information are provided for the sen me-derived single exempt her that
           are expressed significantly in human rotal liver cul.s. Also described are 12,456 single exon nucleic acid probes and 12,020 proteins expressed
            in the fetal liver and their use in methods for detecting gene expression.
            The genome-derived single exon nucleic acids comprise a novel type of
           nucleic acid microarray for verifying gene expression. In addn., methods
           are provided for identifying exons in a eukaryotic genome, and for
           assigning exons to a single gene. [This abstr. record is one of nine
           records for this document necessitated by the large no. of index entries
           required to fully index the document and publication system constraints.].
ŢΤ
           400957-73-5
           RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties);
           ANST (Analytical study); BIOL (Biological study)
                  (amino abid sequence; human genome-derived single exon nucleic abid
                  probes useful for anal. of gene empression in human fetal liver;
L11 ANSWER 10 OF 26 HOAPLMS COPYRIGHT 2013 ACA
ACCESSION NUMBER: 00002:11 Fire Hoapland
DOCUMENT NUMBER: 124:4002
                                                        Human genome-derived single extrand teld avid probes
                                                        useful for analysis of gene expression in human brain
INVENTOR(S):
                                                        Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;
                                                        Rank, David R.
PATENT ASSIGNEE(S):
                                                        Molecular Dynamics, Inc., USA
SOURCE:
                                                        POT Int. Appl., 650 pp. CODEM: FINANCE
                                                        Parent
LANGTAGE:
                                                        English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:
           PATENT NO. KIND DATE
                                                                            APPLICATION NO. DATE
                                                ____
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          WC 2001087278 AD 20010800 WO 2011HMEWET 20010130
W: AB, AB, AM, AM, AM, AD, BA, BB, BB, BB, BY, BY, BD, MA,
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     GB 2361238
                                                        GB 12761238
                                         W1 21 1=12421 1 1 1 1 1
        W: AE, AR, AL, AM, AT, AT, AL, BA, BB, BR, BB, BL, BL,
PRICRITY APPLN. IMFS.:
   A single exon nucleic acid microarray comprising 12,821 single exon nucleic acid probes for measuring gene expression in a sample derived from
    human brain cells is described. These unique emons are within longer
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probe sequences; sequencing confirms the ewapt chem. structure of each probe. Some amplicons have more than one ewon, and some ewons are contained in more than one amplican. Empression, hamal, and functional information are provided for the genume-derived single exon probes that are expressed significantly in human brain. Also described are 12,613 single exon nucleic acid probes and 11,377 proteins expressed in the brain and their use in methods for detecting gene empression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exens to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the decument and publication system constraints.].

412969-90-5

RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study) (amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human brain)

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LII - AMSWER 13 OF 18 HOAFLUS - COFFRICHT COS ACC
ACCESSION NUMBER: 2010:111981 BYARING DOCUMENT NUMBER: 138:11090
DOCUMENT NUMBER:
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Ruman de nome = e e inte a crimare de well, in a rie la regarda per mas useful for analysis or pene expression in human bone

marrow

INVENTOR (S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng;

Rank, David R.

PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA

PCT int. Appl., et pp. donem: FIMMO2 SATRCE:

lanaraar: English FAMILY ACC. MUM. COUNT: 84

FATENT INFORMATION:

PATRICE NO.	EIL	(ATE	APPLICATI N NO.	
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W: AE, AG, AL, AM, AT, AM, AD, BA, BE, BG, WE, BY, BK, CA,
               OB, OU, CO, LE, DK, LM, DC, EE, ES, FI, SH, GC, GE, GH, BU, IC, IL, IN, IS, IE, KE, KG, KE, KE, KC, LC, LK, LR, LI, LU, MA, MC, MG, MK, MU, MW, ME, MC, MC, MC, BL, PT,
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               SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, TA,
               TE, CA, CM, AM, AC, FY, KG, KC, KC, EC, TC, TM

TE, CM, EF, LC, CM, MC, CC, CL, CC, TC, CC, AT, EE,
LE, LE, EJ, FE, FE, SE, LE, LT, LU, MC, CL, ET, SE,
             CH, Y,
                                                                           TE, EF,
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om 2000-14263
     GB 2360284
              73 20021
PRIGRITY APPLN. INFO.:
                                            US 2000-207456P P 20000526
                                            US 2000-608408 A 20000630
                                            US 2000-632366 A 20000803
                                            US 2000-234687P P 20000923
                                            US 2000-236359F P 20000927
                                            GB 2000-24263 A 20001014
                                            WO 2001-US668
                                                             E 50
AΒ
    A single exon nucleic acid microarray comprising 10,114 glague exon
     nucleic acid probes for measuring gene empressilm in a sample derived from
     human bone marrow is described. These unique emins are within longer
     probe sequences; sequencing confirms the exact ohem. structure of each
     probe. Some amplicons have more than one exon, and some exons are
     contained in more than one amplican. Expression, homol., and functional
     information are provided for the genome-derived single exampropes that
     are expressed significantly in human bone marrow. Also described are
      12,898 single exch hubleid abid prokes and 12,616 proteins expressed in
     the bone marrow and their use in methods for detecting gene empression.
     The geneme-derived single exen nucleic acids comprise a novel type of
     nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine
     records for this document necessitated by the large no. of index entries
     required to fully index the document and publication system constraints.].
     402671-83-4
     RL: ANT (Amalyte); BSV (Biological study, unclassified ; FBF (Freporties); AMSI (Amalytical study); BIOL (Biological study)
         (amino acid sequence; human genome-derived single emon nucleic acid
        probes useful for anal. of gene expression in human bone marrow)
DODINERS:
                           1984 1881 - 1
                            Comments in the local ending
TITLE:
                          Human numbers and send their enoughd proteins and
                           antibodies
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                          Rosen, Oraid A.; Barash, Steven D.; Ruben, Steven M.
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Patent English

DOCUMENT TYPE: LANGUAGE: FAMILY ADD. NUM. COUNT: PATENT INFORMATION:

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 US 2000-229509P P 20000905
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US 2000-246523P P
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US 2000-246609P P
US 2000-246613P P
US 2000-249207P P
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polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "musculoskeletal system antigens", and the use of such musculoskeletal system antigens for detecting disorders of the musculoskeletal system, particularly the presence of cancer and cancer metastases. More specifically, 1023 isolated musculoskeletal system-assocd. cDNA mols. are provided encoding novel musculoskeletal system-assocd. polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system assocd, polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

ΙT 384873-95-4P

RL: BPN (Biosynthetic preparation); BSJ (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) amino acid sequence; human musculoskeletal system-specific nucleic

acids and their encoded proteins and antibodies?

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L11 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:763025 HCAPLUS
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DOCUMENT NUMBER: 195:335111

TITLE: Albumin fusion proteins with therapeutic proteins for

improved shelf-life

INVENTOR(S): Rosen, Craig A.; Haseltine, William A. Human Genome Grieness, Inc., UCA PATENT ASSIGNED (S):

SOURCE: FOT Int. Appl., DITE pp.

CODEN: FINND2 DOCUMENT TYPE:

Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: PATENT INFORMATION:

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PATENT NO. KIND DATE
                                       AFFLICATION NO. DATE
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MO DOCIONATO AT LOCATION MO DOCI-VETISES 20010412
M: AE, AG, AL, AM, AT, AT, AU, BA, BB, BG, BR, BY, BG, CA, CH, CM,
CC, CB, CT, CE, CE, CM, CM, CE, ES, FI, GB, GD, GE, GH, GM,
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EP 127,786
          PRIGRITY APPLIED INFO.:
ĀΞ
      The present invention encompasses fusion proteins of albumin with various
      therapeutic profeins. Therapeutic proteins may be stabilized to extend
     the shell-life, and/or to retain the therapeutic protein's activity for extended periods of time in solm., in vitro animor in viv., by a new (val) or ther. fusion to confination the therapeutic protein to all more or a fradment or variant or allumin. The therapeutic postern or proteins may also reduce the need to formulate the protein solms, with large excesses or
      carrier proteins to prevent loss of therapeutic proteins due to factors
      such as binding to the container. Nucleic acid mols, encoding the albumin
     fusion proteins of the invention are also encompassed by the invention, as
     are vectors contg. these nucleic acids, host cells transformed with these
      nucleic acids vectors, and methods of making the albumin fusion proteins
      of the invention and using these nucleic acids, vectors, and/or host
      cells. Thus, plasmid westers are constructed in which DNA encoding the
      desired therapeutic protein may be inserted for expression of the albumin
     fusion proteins in yeast (pPPC0005) and mammalian cells (pC4:HSA).
     Yeast-derived signal sequences from Saccharomyces cerevisiae invertase
      SUC2 gene, or the stanniocalcin or native human serum albumin signal
     peptides, are used for secretion in yeast or mammalian systems, resp.
      Thus, the fusion product of human growth hormone with residues 1-387 of
     human serum albumin retains essentially intact biol. activity after 5 wk
     of incubation in tissue culture media at 37.de mee., whereas resumbinant
     human growth homone used as control lost its $1.1. As it by in the first week. Although the potenty of the albumin rush in proteins is slightly
     lower than the untused counterparts in rapid bloassays, their bull.
     stability results in much higher biol. activity in the longer term in
     vitro assay or in vivo assays. Addnl., the present invention encompasses
     pharmaceutical compns. comprising albumin fusion proteins and methods of
     treating, preventing, or ameliorating diseases, disorders or conditions
     using albumin fusion proteins of the invention.
     369644-05-3
     RI: FRF (Properties)
         (unclaimed protein sequence; albumin fusion proteins with therapeutic
         proteins for improved shelf-life;
REFERENCE COUNT:
                                 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS
                                  RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT
L11 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:582023 HOAPLUS
TANNENT NAMER:
                            138:173431
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                           Nuclein wolds and their on mied polypoptides from
                           human bone marrow
                           Ford, John E., Poyle, Bryan I., Tang, Y. Ton, Liu,
INVENTOR S':
                           Chenghua; Asundi, Vinci, Chou, Fina; Mae, Adina;
                         Ben, Feigan, Drmanas, Fai is fr.
Hyseg, Ins., TrA
FOT Ins. Appl., st. pg.
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US 2000-496914 A 20000203
US 2000-598075 A 20000620
US 2000-620325 A 20000719
US 2000-250593P A 20001130
WO 2001-US3782 W 20010205
PRIORITY APPLN. INFO.:
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The present invention provides a collection or library of 94 nucleic acid AΒ contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The cDNA libraries are from human bone marrow sources and nearest neighbor sequence himsh gives are provided. The invention also relates to the proteins end to by such polynomeral along with therapeutic, diagnostic and reveal to brillion for these polynucleotides and proteins.

ΙT 353568-97-5 354113-34-1

RL: ANT (Analyte); BOS (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES

(amino acid sequence; nucleic acids and their encoded polypeptides from human bone marrow'

LII ANSWER 17 OF 26 HOAFLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:566854 HCAPLUS

DOCUMENT NUMBER: 135:163414

TITLE: Human nucleic acids and their encoded proteins and

antibodies

INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.

PATENT ASSIGNEE'S': Human Genomé Soiences, Ins., USA

SOURCE: FOT Int. Appl., 532 pp. .. NOTEM: FIRM:

DOCUMENT TYPE: Fatent LANGUAGE: English

FAMILY ACC. NUM. COUNT: FATENT INFORMATION:

PATENT NO.	RIND DATE	APPLICATION NO. DATE
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	A	W 0 1-0/1916
W: AE, AR,	āl, an, at, an,	CO, BA, BB, BR, BR, BT, BD, CA, CH, CM,
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	+-,, .2, .2,	KE, KG, KE, KE, KZ, LC, LK, LR, LS, LT,
	and the second of the second	M, MM, MM, MO, MO, EL, ET, EO, RU,
ST, SE,	50, 80, 80, 80,	TI, TM, TB, TT, TZ, TA, CG, CS, TC, TN,
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                                             RW: GB, GM, KE, LJ, RW, ME, JD, SL, JD, JE, JK, ES, F1, FB, JB, JF, JE, JT, BJ, DF, DS, DI, TM, GA, MI, GW, ML, AV AVIII AV AVIII AV AVIII AV AVIII AV AVIII AV AVIII AV
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US 2000-179065P P
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US 2003-2363678 F 200000927

US 2003-2464768 F 20000106

US 2003-2465258 F 20001108
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US 2000-249214P
US 2000-2492165P
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US 2000-2492690P
US 2000-251988P
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US 2000-225758P P .00000814
US 2000-226868P P .00000822
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US 2000-225924P P .00000901
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US 2000-234413P P .00000905
US 2000-234423P P .00000901
US 2000-234274P P .00000901
US 2000-234274P P .00000901
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US 2000-237039P P (00)1) 2
  US 3000-137040P P 100010 2
  US 2000-141735P P .0011) 0
 US 2000-141808P P . 3001.0
US 3000-14461P P 100011 1
 US 1000-149238P P 10001117
 US 2010-151830P P 100001208
US 2000-031868P P 20001208
US 2000-151869P P 20001208
 US 1001-764859 A2 10010117
US 2001-764863 B1 .0010127
WO 2001-US1346 W ..0010117
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The present invention relates to novel human polynucleotides and the polypeptides encoded by these polynucleotides, and the use of such polypeptides for detecting disorders. More specifically, "9 isolated human cDNA mols, are provided encoding novel polypeptides. Antibodies that bind to these polypeptides are also provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing the novel human polynucleotides and/or polypeptides. The invention further relates to diagnostic and therepoutes methods useful for diagnosing, treating, preventing and or progressing disorders and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying aganists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compass, for inhibiting the producing function of the polypeptides of the present invention.

IT 353554-69-5, Protein (human clone HFIEC13)

RL: BSU (Biological study, unclassified); PFP (Properties); BIDL (Biological study)

 'protein sequences; human nucleic acids and their encoded proteins and antibodies;

REFERENCE COUNT:

2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L11 ANSWER 18 OF 26 HCAPLUS COFYRIGHT 2003 ACS ACCESSION NUMBER: 2001:397059 HCAPLUS DOCUMENT NUMBER: 138:139831 TITLE: 3ens of Bhus numberily
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endymes if the synthesis of polyunsaturated fatty
                                                                                                      acids and lipids
     INVENTOR 8 :
                                                                                                       lerchl, Jens; Renc, Andreas; Ehrhardt, Thomas; Reindl,
                                                                                                     Andreas; Cirpus, Fetra; Bischoff, Friedrich; Frank,
                                                                                                      Markus; Freshi, Aneste; Dumenia, Elke; Schmidt,
                                                                                                      Ralf-Michael; Rockt, Rulf
                                                                                                   Basi Flant Colonse Smbh, Sermany
FCT Int. Appl., 113 pp.
CODEM: FINNES
    PATENT ASSIBLE ::
    SOURCE:
    DOCUMENT TYPE:
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   LANGUAGE:
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                     WO 2001036484 A2 20010531 WO 2001038484 A3 20011101
                                                                                                                                                                       WO 2000-EP11615 20001122
                                     W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, BZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
                                                     HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
                                                     LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
                     LU, LV, MA, MU, MG, MK, MN, MW, MX, MZ, NG, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TU, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TU, TM

RW: SH, GM, KE, LS, MW, MC, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, ML, FT, SE, TR, BF, BU, CF, CG, CI, CW, CM, CM, CW, MI, ME, ME, CM, TI, TI

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                     AU 2001019745 AE 20010614 An 1001-1004 IIII
BR 2000015905 A 20020806 FR 2000-15901 20001101
EP 1282713 A2 20030212 EP 2000-979617 20001122
                                     R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
                                                     IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
  PRIORITY APPLN. INFO.:
                                                                                                                                                               WO 1999-EP9108 W 19991125
                                                                                                                                                               WO 2000-EP11615 W 20001122
                  Isolated numbers acid mols., designated LMRP numbers acid mols., which
                    encode novel LMRPs from e.g. Physoliticalla patents are described. The
                     invention also provides antisense nucleid adid mols., recombinant
                     expression vectors contg. LMRF nucleic acid mols., and host cells into
                    which the expression vectors have been introduced. The invention sill
                    further provides isolated LMRPs, mutated LMRPs, fusion proteins, antigenic
                    peptides and methods for the improvement of the prodn. of a desired compd.
                    from transformed cells, organisms or plants based on genetic engineering
                    of LMRP genes in these organisms.
                    343286-49-7
                    R1: BUT (Biological use, unclussified); FRF (Properties); Biological study); USES (Uses)
                               /amino abid sequence; genes of Physicmitrella patens encoding homologs
                               of encymes of synthesis of polymesatd, fatty acids and lipids'
THERE ARE TOTTED REFERENCES AVAILABLE FOR THIS
RECTED. ALL CITATIONS AVAILABLE IN THE RE FORMAT
 REFERENCE COUNT:
LII ANSWER 1 - OF 10 HOAFIUS OF BYBIGHT . O AND ACCESSION NUMBER: 10 NOT 10 HOWEVER . O CONTROL OF WHICH THE CONTROL OF SEQUENCE ACCESSION ACCESSI
                                                                                                Sequence-determined DNA fragments and corresponding
                                                                                                encoded polypeptides from corn and Arabidopsis
Alexandrou, Mickolai; Brower, Myacheslau; Chen,
INVENTOR(S):
                                                                                                 Mianfend; Subramanian, Gopalakrishnan; Troukhan, Maxim
E., Cheng, Liansheng, Cumas, J.
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PATERIT AND RIBE IN : Negers In ... NOW. 800808:

Eur. Fat. Appl., Herry. DIED: FERRIS Patent

English

DOCUMENT TYPE: LANGUAGE: FAMILY ACO. 100M. (20100): PATFUT INFORMACION:

FATENT NA. RINL TATE ASSLITATION NO. DATE

EF 1033400 A2 20000906 EF 2000-301439 20000225

F: AT, BE, TE, DE, DK, ES, FE, GE, GR, IT, LI, LU, NL, SE, MC, PT, LE, SI, LT, LV, FI, RO

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 US 1999-134768P F 19990518
US 1999-134941P F 19990519
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AB The present invention provides DNA mols, that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA nols, are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence cr as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis LMA is used in the present expt., but the procedure is a general one. Frotocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA13316218528Q necessitated by the large no. of index entries required to fully index the document and publication system constraints.).

TΤ 302645-65-4 302645-66-5

FL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); CCCU (Occurrence); USES (Uses)

(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

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L11 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2003 ACS
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DOCUMENT NUMBER:

ACCESSION NUMBER: 2000:754707 HCAPLUS

INVENTOR(S):

133:318296 Sequence-determined DNA fragments and corresponding

TITLE:

encoded polypeptides from corn and Arabidopsis

Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim

E.; Zheng, Liansheng; Dumas, J.

PATENT ASSIGNEE(S):

SOURCE:

Ceres Inc., USA Eur. Pat. Appl., 339 pp.

CCDEN: EPNNOW

DOCUMENT TYPE: LANGUAGE:

P - + - - - + Englist.

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND DATE	AFFLICATION NO. DATE
EP 1033408 B: AT, BE, 1E, ST,	A2 20000906 CH, CE, CK, ES, FR, LT, LV, FI, BC	EF 2000-301439 20000025 38, GR, IT, LT, LT, ML, SE, MO, FT,
0A 0300690 0A 0300818 EP 1088728	AA 20000908 AA 20001006 AC 20001109	0A 2000-2300692 000000225 0A 3000-2302828 20000406 EP 2000-303770 20000504

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B: AT, BE, CH, LE, LK, ES, FB, GE, GE, LT, LE, LM, ML, SE, MM, PT, LE, SI, LT, LW, FI, RO

EF 1[54]60 A2 A1111112 EF 2111-614161 21111517
- 2000 AL 20000122 EF 2000-314161 20000817

R: AT, RE, CE, CE, CE, ES, EB, GE, CE, LT, LT, NL, SE, MC, ET,

LE, RI, LT, LT, ET, EC

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The present invention provides INA mols, that constitute fragments of the genome and coulds from Dea mays mays HYPRID SHED #35Ald and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides enough thereby. The DMA rols. The useful for specifying a medic pardick in wells, which is a spromiter or as a protein ordinate sequence or as as WTB or as a set promiter or as a protein ordina sequence in an another than it as permited for sequence, and are such as the expression of a general massine, in a non-clinic the expression of a general arc tools for genetic mapping, resoluting or isolating if entitied or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hypridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CALPATE DIST. to describ to day the large no. of index entries required to fully undex the accument and purification system constraints.]. 302411-42-3 302411-43-4 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); FRF (Froperties); BIOL (Biological study); OCCU (Codurrende); USES (Uses aming abili sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis;

LII ANSWER 21 OF 26 HOAPLUS COPYRIGHT 2 15 ACS

ACCEDSION NUMBER: 137:31*6*36

TITLE: Sequence-determined DNA fragments and corresponding

encoded polypeptides from corn and Arabidopsis Alexandrov, Nickolai; Brover, Vyacheslav; Chen,

INVENTOR(S):

Kianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim

E.; Zheng, Liansheng; Dumas, J.

PATENT ASSIGNEE(S): Ceres Inc., USA

SOURCE:

Eur. Pat. Appl., 339 pp.

CODEN: EPHNEW

DOCUMENT TIPE: Fatent LANGUAGE: English

FAMILY ACC. NUM. COUNT: 16

PATENT INFORMATION:

PA:	TENT NO.	KIND	DATE			ATION NO.		
ĒF	1033405 R: AT, IE,			FR, GF	EF 2000	1-301439 T, LI, I		r
CA CA EP	2300692 2302828 1055728	AA AA AA AC			CA 2000	-1300692 -2302828 -303770	20000408	
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EP	1054060 R: AT, 1E,	A2 BE, MH, MM S1, MT, MM	, IK, EJ,	FR, H	RF 2000 7 - R, I	-: 4161		, F,
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US 1999-130724F
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TS 1999-138094P F 19990608
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The present invention provides DNA mols, that constitute fragments of the genome and cDNAs from Dea mays mays (HYBBID SEED #38A10) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides enough thereby. The DNA mols, are useful for specifying a sene product in cells, either as a promoter or as a protein hoding sequence of as an UTB or as a starmination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the empression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present empts, but the procedure is a general one. Protocols are provided for Southern hybridications and transformation of carret cells. [This abstr. record is one or 15 records supplemental to CA1351d1151c1, necessitated by the large not of index entries required to fully index the document and publication system constraints.].

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LII ANSWER 22 OF LC HOADLIS CHEMPISHT 2019 AND ACCESSIVE NUMBER: USING HOADLIS CHEMPISH BOADLIS COUNTY NUMBER: USA:C40.5

TITLE: Cloning and expression of a gyne percoding a putation

chloroplast comegate ratty abid desaturate of marine

Mlamy'im nas

Miyasaku, Hitoshi; Tanaka, Satushi; Kanabushi, Harub Tech. Res. Cent., The Kansai Electric Stwer (1., 11-0 Nakoji r-chume, Amagasaki, Hyur, 11-1404, Jagan Flant Birtechnol ny Tokyo (2001, 2001, 11-101) COLEU: FIE186; INC AUTHOR(3): CORPORATE SUURCE:

SOURCE:

PUBLISHER: Japanese Society for Plant Cell and Molecular Biology

DOCUMENT TYPE: Journal LANGUAGE: English

AB A dDNA encoding putative chloroplast .omega.6 fatty acid desaturase was isolated from a cDNA library of marine Chlamydomonas sp. strain W-80. The mRNA level of this gene under various conditions of stress was examd, by northern plotting anal., and the transcript level was increased under a cold-stressed [4.legree.] condition.

307998-10-3

RL: PRP (Properties)

(amino acid sequence; cloning and expression of a gene encoding a putative chloroplast .omega.6 fatty acid desaturase of marine Chlamydomenas)

L11 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2:03 Acs

ACCESSION NUMBER: 1998:773005 HOAPLUD

DOCUMENT NUMBER:

TITLE: Designering the blol gy of Myr parterium traveroulosis

from the complete genome sequence. (Erratum to

document dited in CA129:77224]

AUTHOR [8]: Cole, S. T.; Brosch, R.; Farkhill, J.; Garnier, T.;

Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier, K.; Gas, S.; Barry, C. E., III; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, Hamlin, M.; Molean, J.; Moule, S.; Murphy, M.; Coliver, K.; Margh, A.; Molean, J.; Moule, S.; Murphy, M.; Cliver,

K.; Osborne, J.; Quail, M. A.; Rajandream, M.-A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, J.; Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.;

Whitehead, S.; Barrell, B. G.

CORPORATE SOURCE: Sanger Cent., Welldome Trust Genome Campus, Hinwton,

TRICIDA, TW Lature Colemn Clare, FAR For , 18 - 18 COLEMN MANUAC, Tests: Colemn Macmillan Magazines S YIROR:

FUBLISHER:

POCUMENT TYPE: LANGUAGE: Journal English

Table I was published with some symbols missing; the correct wersion can be found at http://www.sanger.ac.uk/ac.i/is/diven here. In Fig. 1, Becgge was imporrectly labeled as call 37 instead of fabil. Two of the genes for mysolyl transferases were inverted: By 11.75 end declarities for and not military and selections of the properties of th designated fbpD. The sequence of FbDD40 from M. boris BCG-Pastern

presented in Fig. 6) was interpret and should have which a leave th deletion instead of con-208786-02-1 BL: BRE Properties deciphering the kill. If Myssika terium takersulssis from the samplete genime sequenio (Erratumi)

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AUTHOR & :

from the complete genome sequence
Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.;
Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier,
K.; Gas, S.; Barry, C. E., III.; Tekaia, F.; Badcock,
K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor,
R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krosh, A.; Molean, I.; Modle, S.; Murphy, I.; Oliver, K.; Dehorne, I.; Josil, M. A.; Fagandress, M.-A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelten, J.; Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.;

Whitehead, S.; Barrell, B. G.

CORPORATE SOURCE: Sanger Cent., Welliume Trust Genome Campus, Hinwton,

CBIÓ ISA, UK

Nature (London) (1995 , 393 6685), 837-844 CODEN: MATURS; ISSN: (196-1836 SOURCE:

Marmillan Magazines FUBLISHER:

DOCUMENT TYPE: Journal LANGUAGE: English

AB Countless millions of people have died from tuberculosis, a chronic infectious disease caused by the tubercle bacillus. The complete genome sequence of the best-characterized strain of Mycobacterium tuberculosis, Holky, was detd. and analyzed in order to improve our understanding of the biol. of this slow-growing pathogen and to help the conception of new prophylactic and therapeutic interventions. The genome comprises 4,411,529 base pairs, contains around 4000 genes, and has a very high G+C content that is reflected in the biased amino acid content or the proteins. M. tuberculosis differs radically from other bacteria in that a very large portion of its coding capacity is devoted to the prodn. of enzymes involved in lipogenesis and lipolysis, and to 2 new families of glycine-rich proteins with a repetitive structure that may represent a source of antidenic variation.

208786-02-1

BL: PBF Properties

camino acid sequence; decuprering the colour Mysteastering

tuberquiosis from the complete genome sequence:

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 25 OF 26 HORFIUS COFFRIGHT 2013 ACS

1998:61353 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 125:214937

l mina di a gene ion diloroplast lomean. I desaturase

si a green alga, Chlangdomenas reinhardtii

AUTHOR S : Sate, Moribire; Fullwara, Shoke; Kawasuchi, Akihike;

Tsuzuki, Mikis

School of Life Science, Tokyo University of Pharmady and Life Science, Tokyo, 192-13, Japan Tournal of Biochemistry Tokyo (1990), 180 %, 184-1830 CORPORATE SOTROR:

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1 JOUNEUT TYPE: Journal LANGUAGE: English

AB - A gene for chloroglast .omega.6 desaturuse, which catalynes the desath. .f monitencia to dienkia acids in chloroplasts, was isolated from Chlamydomonas reinhardiii. Peverse Transfriptaseep Tyrerase saan reaction was first yerr inclimitatio .la name ta carriera e como a carrier is a unit of the row a unit application of pure an article of including plants and liberary and selection of the property and the selection of the property and the selection of himilogous to these desaturases, was used as a proce for spreening cDNA and genemic DNA libraries of C. rwinhardtii. The cDNA plone of 2.2 kb obtained contained an open reading frame encoding a protein of 424 amino abids with a putative mol. mass of 48.4 kDa, the amino abid sequence of which showed 46-81 homel, to those of higher plant plastid .omega.6 and tyunobatterial .IFLTA.11 desatureses. Introduction of the cloned genomic counterpart of this cDNA, designated as dese, into a Chlamydomonas mutant with defects in chloroplast .cmega.6 desath, and in the activities of photosystems I and II (PSI and PSII) complemented the desatn. mutation, indicating that the dese gene codes for Shloroplast .omega.6 desaturase. The complemented strains did not recover from the photosynthetic lesions, but showed lower PSII activity at 45.degree, than the desath, mutant, proving that the photosynthetic lesions in hf-9 are not caused by the desath. mutation, and that the lowered unsath. Level of chloroplast lipids in the mutant is responsible for the expression at this night top. of FALT activity, one of the thylakoid membrane functions.

204279-00-5

RL: BSU (Biological study, unclassified ; FRP [Properties]; BIOL (Biological study

(amine acid sequence; cloning and sequence of gone deso for chloroplast .omega.6 desaturase of a green alga, Chlamydomonas reinhardtii)

L11 AMSWER 26 OF 26 HOAPLUS COPYRIGHT 2013 ACS 1998:936841 HCAPLUS ACCESSION NUMBER:

124:47157 DOCUMENT NUMBER:

TITLE: Identification and functional analysis of the transfer

region of plasmid pMEA300 of the methylotrophic

actinomycete Amycolatopsis methanolica

AUTHOR [S]: Vrifbloed, J. W.; van der Put, N. M. J.; Diikhuizen,

L.

Dep. Microbiology, Univ. Groningen, Haren, 9751, Neth. Journal of Bacteriology (1995), 177(22), 6499-505 CODEN: JOBAAY; ISSN: 0021-9193 CORPORATE SOUPCE:

SOURCE:

PUBLISHER: American Society for Microbiology

DOCUMENT TYPE: Journal LANGUAGE: English

- Amydolatopsis methanolida dontains a 13.3-kb plasmid (pMHA300) that is present either as an integrated element or as an autonomously reglicating plasmid. Conjugational transfer of pMEASCO results in post formation, cones of drawth inhibition that he who apparent when a family-ranging denor cells details in a conflict came optace. His wine receptor cells. A 6.2-kb pMHA300 IMA region specifying the functions of conjugation and pook formation was sequenced, revealing 10 open reading frame.s. This it the first sequence of the transfer region of a plasmid from a nonstreptomy sete a minomy sete. No clear similarities were found between the deduced sequences of the 10 putative Tra proteins of pMEA300 and those of Streptomy ses plasmids. All Tra proteins of pMEA300 thus may represent unfamiliar types. A detailed mutational anal, showed that at least four individual proteins, Tradoly,44+ Cal, TraHoly,6+8 la , TraHoly,6+8 la , Tradol4+8 la , Tradoly,6+8 la , Tradoly,6+ pMFA: C. Their disruption resulted in a Slear redn. in the conjugational transfer the quentiles, randing from (5.2 stimes, 101)-feld (Trad) to (2.3 Trimes. 178 -fold Trad , and in reduced prok sides. At least two purative proteins, TraB (17,686 Da) and TraB (31,440 Da), were shown to be

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 Experimental and calculated property data are now available. See HELP
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RELATED SEQUENCES AVAILABLE WITH SEQLINK

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OTHER NAMES:

CN 104: PN: US20020165137 SEQID: 104 claimed protein

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uncommon	5 1 1 - P 4	_	-		
************	Asa-12 H	-	-		
uncommon	Aaa-141	-	_		
un demmer.	Aaa-14 ⁸	_	_		

SQL 175

SEC 51 ACRIRAGERA GOTGOWYAME FOOSWEDOLA SUMPURENUS USORFWEWSA

BITS AT: 66-11

FELATED SECTEMBED AVAILABLE WITH SEQUINK

BEFERENCE 1: 170:340800

LB AMBWER 7 OF BE RESISTED CORNETORY LIFE ACS

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487684-48-9 RESISTRY
    Protein (Mycoba terium tukenculosis strain (1001161 gene MT6166) (1801) (CA
ON GenBank AESSCRis-derived protein RESISRIA
    1 MITERSPEA : BYAR SORELE REPETWIVEH BTHALLLERI ITAGELLACO
. E.
HITS AT:
         26-31
**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 137:017411
   - ANSWER & OF BE REGISTED MIDDLESS AV
    440301-84-8 REGISTRY
   - Protein (Methanosardina madei strain Goel dens MMC191) - 901) - (CA INDEX
    NAME)
MTHER MAMES:
ON GenBank AE013459-derived pricein 30 U1908783
30L
    181 LOSRYTFFMA SLIFGILWOL WHEFLIFUKO MYQYEIFHEN IWYAUNFFVG
SEQ
HITS AT:
         168-173
REFERENCE 1: 137:74267
13
   ANSWER 9 OF 38 REGISTRY COPYRIGHT 2003 ACS
   437141-30-5 REGISTRY
    6-Phosphogluconolactonase (Arabidopsis thaliana clone RAFL05-08-012
     (R0988) gene At5g24400) (901) (0A INDEX NAME)
OTHER NAMES:
   GenBank AF370305-derived protein GI 13878085
SQL 219
    51 GGSLIKSLRK LVESPYJDSI DWARWHFFWJ DERJYFKWHD DSWYKLAYDS
SEQ
HITS AT: 72-77
REFERENCE 1: 137:88:49
   ANSWER 10 OF 39 REGISTRY COPYRIGHT 1003 ACS 437115-91-8 REGISTRY
    Protein (human clone US20020048763-SEQID-44744 exon-encoded fragment)
     (9CI) (CA INDER NAME)
OTHER NAMES:
am - 4008: FM: US20020049063 SEQID: 44044 blaimed protein
        1 NIIQLLEGFI HHGAWQMAWR AWHFKFILME SIEGLR
3EQ
                             == ====
HITS AT:
         19-24
**BELATED PERCENCES NUNTLABLE WITH SERLINK**
REFERENCE 1: 187:04443
   ANSWER II OF BE BERIEFE MIRELED - FAV
    41.9.4=>>=0 BERINTEY
    L-Arginine, leasparagingleteischer gleleischer glebealdramingleieler glebe
    led by lete, alpha. Epidtangi bly by lete, hongial any lete isolow by letehist i dy lete
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histidylglycyl-i-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-
     tryptophyl-1-arginyl-1-alanyl-1-tryptophyl-1-histidyl-1-phenylalanyl-1-lysyl-1-phenylalanyl-1-leusyl-1-methionyl-1-alpha.-glutamyl-1-
     seryl-L-isoleupyl-i-.alpha.-glutamylglybyl-L-leubyl- (901) (CA INDEX
OTHER NAMES:
CN 98%: PN
CN Protein
     933: PN: W00157273 SELTO: 34985 blaimed protein
Protein (human blone W001057273-85LID-34985 emon-encode: frameno
SEC
          1 NIIVILEGET HEGANQMANE AMHERECCHE COPPUR
                                44 7 5 5 5 5
HITS AT:
            19-14
**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 136:351357
     ANSWER 12 OF 38 REGISTRY COPYRIGHT 2003 ACS
KM
     41:969-90-5 REGISTRY
     L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-
ΩN
     le cyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-
     histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-
     tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-
     lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-lalpha.-glutamyl-L-
     seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX
     NAME)
FIHER NUMES:
ΞN
     35: PN: W00157275 SEQID: 33858 claimed protein
     Protein (human brain clone W00157275-SEQID-33858 exch-encoded fragment)
ΞN
COL
SEO
         1 NIIQLLEGFI HHGAWQMAWR AWHFKFILME SIEGLE
HITS AT:
           19 - 24
**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 136:320295
....3
     ANSWER 13 OF 38 REGISTRY COPYRIGHT 2003 ACS
EN
     40:874-66-6 REGISTRY
     Protein (Methanosarcina acetivorans strain C2A gene MA1162) (9CI) (CA
CN
     INDEX NAME)
OTHER NAMES:
     Ger.Bank AE010783-derived protein GI 19914997
SEO
       151 LQSRHTFFTA SIFFSILWSL WHEPLIFVNN MYQYEIFHEN VWYAVNFFVS
HITS AT:
           168-173
REFERENCE 1: 136: 59774
13
     ANSWER 14 OF 38 REGISTRY COPYRIGHT 2003 ACS
    402671-93-4 REGISTRY L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-
EN
     leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-iscleucyl-L-histidyl-L-
     histidylglycyl-L-alanyl-L-tryptcphyl-L-glutaminyl-L-methicnyl-L-alanyl-L-
     tryptophyl-L-arginyl-L-alanyl-i-tryptophyl-L-histidyl-L-phonylalanyl-L-
     lysyl-l-phenylalanyl-l-isoleu yi-l-leubyl-l-methionyl-l-lalpha.-glutamyl-l-
     skrýlelelskikurýlelelalphakejúsamylglyfylelelebylf (901) f ca ímpsm
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JIHER NAMES:
ON REE: PN: WOTTETZTO SELIC: 34819 Staimed profession
     Protein (human bong marrow of he William For, ID-818) which-end by
SEL
         1 NII, LLEGFI HEGAW, MAME AWHEKFILME GIEGLK
BITTO AT:
         12-24
**RELATED SEQUENCES AVAILABLE WITH SECLIME**
REFERENCE 1: 136:22" 4 %
13
     ANSWER 15 OF 36 REGISTRY COFYRIGHT 2006 ACC
     400957<del>-</del>73-8 REGISTRY
\mathbb{R}\mathbb{N}
     Protein (human fetal
                        liver blone M00157277-SEQID-38528 emon-enhaded
     fragment) (901) (CA INDEM NAME
OTHER NAMES:
     528: PN: W00157277 SEQID: 33818 Himmain: Thin
CM.
SCI
         1 NIIQALEGET HEGAM, MAME AMBEKETIME SIRBLA
SEQ
HITS AT:
          19-24
**RELATED SEQUENCES AVAILABLE WITH SEQLINK**
REFERENCE 1: 186:195268
13
    AMBMER 10 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN
    400696-91-5 REGISTRY
CN
    Secretory protein (human clone HNNBM45 53-amino acid precursor) (9CI) (CA
     INDEX NAME)
OTHER NAMES:
    96: PN: W00216390 SEQID: 98 claimed protein
NTE
type
        ----- location -----
.
undormon Aau-82 -
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SQL 53
SEQ
        1 MVFLSHLEGT KRIFILLALI WAGWHESYMF ADAWYDEGIE DAYNARYLSI
                              ===:-:
HITS AT:
          21-20
**RELATED SEQUENCES AVAILABLE WITH SEQUINK**
REFERENCE 1: 130:196341
    AMSWER 10 of 38 REGISTRY COPYRIGHT 2003 ACS 400664-75-0 REGISTRY L-Argining, L-asparaginyl-L-isolousyl-L-isolousyl-L-glutaminyl-L-leucyl-L-
1.3
RN
    Toucyl-L+. Als hall-glut an yl glycyl-L+s henyl alanyl-L+is sloneyl-L+hist i ayr1-z-
histidyl glycyl-L-tal anyl-L-tryp os hyl-L-glut aminyl-l-no j hignyl-t- alahyl-t-
    OTHER NAMES:
  - Gef: FM: W. Mindel dw. Di: Gen. Glass-Egantein
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S #941% 9 19 811.414

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- Protein chuman placenta clone W. 11572/2-2E_II-34232 ewon-encode: fragment,
SQL
    36
SEÇ
    1 Naigliegel Hegangwane Ameryfilme Giegla
                          ======::::
HITS AT: 19-24
**BELATED CE, CENCER ALALIABLE WITH CE, LINE**
REFERENCE 1: 1:0:227:1:
    LANGUER 18 OF 38 REGISTRY CORPRISET LOSS AND
    394342-96-2 REGISTRY
RN
   SPERMIDINE SYNTHASE TRANSMEMBRANE PROJECTS (Falstonia solanabearum strain
           dene speE11 90I, CA HULEM NAME
STHER NAMES:
    GenBank Al640 s4-derived protein 41 1 4:1:1;
SEQ 181 VSLLEPLVLA PREGEVRICE LEGEONIATA VWILWHERAE LGESARERGA
HITS AT: 182-187
REFERENCE 1: 136:145954
1.3
   AMSWER 19 OF 38 REGISTRY COPYRIGHT 2103 ACS
RN 394342-70-2 REGISTRY
CN SPERMIDINE SYNTHASE PROTEIN (Ralstonia solanacearum strain GMI1000 gene
    speE2) (9CI) (CA INDEM NAME)
OTHER NAMES:
CN GenBank AL646084-derived protein GI 17431779
SOL
    151 EVSRVLTEDY LGALAVSILE PLVLAFRIGE VRIGELEGIG MTATAVMILM
SEO
      201 HFRAELGISA RLEGAMAMBA GMUGAALLAG PAAGDEUTEW SERALEGDEI
HITS AT: 197-202
REFERENCE 1: 136:145954
   AMSWER 00 OF 38 REGISTRY COPYRIGHT 2003 ACS
13
RN 354873-95-4 REGISTRY
CN Musculoskeletal-associated antigen (human clone HFIEC13-883185 fragment)
    (9CI) (CA INDEX NAME)
OTHER NAMES:
    1147: PM: W00155367 SEQID: 1158 plaimed protein
type ----- I matim. ---- incomigning
_____
undommen. Assa-9e
             A44-95
undemmet.
undermer.
             An i-104
                            -
uncommen
             Aaa-141
             - Asa-140
2<u>,1</u> 11
VEQ - F1 A, F1 FA HBA GUT H WOAWH F3 A WE WIA L WASHE HIVS TO FEMEWOA
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Element 41

HITS AT: 60-71

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**FELATED OR, CENTER ADALLARDE DITE OF, COOP**
REFERENCE 1: 15%:68284
   AMSWER 21 OF 38 REGISTER COPYRIGHT AND ACC
   369644-15-3 BEGISTRY
    ST&: FM: WCCITTIST CEDIA: 1841 unclaimed protein (BCI) — CA INCEM NAME
_______
type
                                       - describtion
______
undermon Adde50 -
______
SOL 53
   1 MUFLSHLFGT KRLFULLALI WASWHFSYMP ADAWUDFGIP DRYLQAYLSI
HITS AT: 21-26
**RELATED REGIENCES ARELIANDE WITH RELIGIES.
REFERENCE 1: 135:335111
13
   AMSWER 22 OF 38 REGISTRY COPYRIGHT 2013 ACS
    354113-34-1 REGISTRY
RN
CN
    L-Phenylalanine, L-methionyl-L-glutaminyl-L-leusyl-L-prolyl-L-isoleusyl-L-
    tryptophyl-L-leucyl-L-histidyl-L-leucyl-L-seryl-L-seryl-L-tyrosyl-L-
    isoleucyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-tryptophyl-L-his idyl-L-phenylalanyl-L-arginyl-L-threonyl-L-methionyl-L-alpha.-glutamyl-L-leucyl-
    L-isoleucyl-L-seryl-L-alanyl-L-seryl-L-valyl-L-leucyl-L-seryl-L-valyl-L-
.alpha.-aspartyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucylglycyl-L-leucyl-L-
    leucyl-L-tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN
    176: PN: WO0157187 SEQID: 176 blaimed protein
CN
    Bone marrow-specific protein (human clone WO0157187-SEQID-176 precursor)
SQL
       1 MQLFIWLHLS SYLWLIWHER TMELISASVL SVOLLILGEL YKF
SEQ
                    _____
HITS AT: 14-19
REFERENCE 1: 135:163431
13
   AMSWER 13 OF ARTRED ACTION OF BYRIGHT CORRESPONDED
   353509-07-5 KR 113TFY
333
   Bone marrow-specific protein (human blone WU/167167-68/10-364
    contig-encoded precursor (901) (0A INDEM MAME
OTHER NAMES:
    361: PM: W00157137 SEQID: 364 plaimed protein
______
            ----- logation ----- description
_____
undermon Ala-33 - - -
______
SQL 96
   El EXEMPLETAL HISSHALLY HERIXELISH CHISTRILL GILINE
SEÇ
HITS AT: FT-TL
REFERENCE 1: 180:180:181
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- ANSWER WAR OF HE REGISTER FOOFFEIGHT 2013 ACC opoly4-we-5 REGICTRY - Protein - Numan Filma HFIEF137 (901) - CA INDEM NAME CTHEEL MARKET: -94: EN: M00108444 SEQIN: 104 blaime: rectoin NIE type ----- location ------ des mintion Aas= 26 Aas= 24 Ass=111 Ass=1111 undommor. Grandraner. A 4 4 = 1 4 1 A 4 4 = 1 4 1 And the second of a Company of the compan SEQ 51 AQRIRAGHRA GGTGCWGAWH FSGSWRGSLA SVGPVPPNVS VSQPFXFXSA -----HITS AT: 66-71 **FELATED CERCENCED AVAITABLE WITH SENTING** REFERENCE 1: 135:163414 13 ANSWER 25 OF 39 REGISTRY COPYRIGHT 2003 ACS RN 343286-49-7 REGISTRY Protein LMRP (Physcomitrelia patens clone 55_ck5_b04fwd lipid metabolism-related) (9CI) (CA INDEX NAME) OTHER NAMES: -241: PM: M00139541 SEQTO: The blaimer protein SOL 51 PATKTLMELG MGPLREWASI GHWLLWHEDL SKYRESEKPR VKISLAAVEA SEO HITS AT: 73-78 REFERENCE 1: 135:19831 1.3 ANSWER 26 OF 35 REGISTRY COFFRIGHT 2003 ACS 307998-10-3 REGISTRY Desaturase, fatty acid .cmega.6-(Chlamydomonas strain W-80) (9CI) (CA INDEX NAME: 352 SEO 201 QEKMKDWNGV TSALFKEFIG TELKLWASVG HWAIWHEDLN KYTEKQRERV HITS AT: 131-237 **RELATED SEQUENCES AVAILABLE WITH SEQUINK** REFERENCE 1: 134:2473 ANSWER AT OF 39 REGISTRY COPPERISHT LOSS AND 1.3 302645-66-5 RESTATE Protein Arabity sis thalland the News (14.14) with the finite many THER MANEET: CN - 969: FN: EBICAMACH SEQUE: Comes millarmed protein 8.11 256 SE, 81 BRILKOLAK LUESERULAL LWARWHERWU DERUUFADHO DEWYKLANDS _ = = -: .:

HITT AT: "L-"T

**RELATED SEQUENCES AVAILABLE WITH SEQUENCES

REFERENCE 1: 133:318297

L3 ANSWER 28 OF 38 REGISTRY COFYRIGHT 2003 AGS

RN 302645-68-4 REGISTRY

ON Protein Arabidopsis thaliana blune Deres 21421400 ROT CA DW EW DAME

OTHER MAMES:

ON 968: PN: EP1033408 SEQID: 60968 plaimed protein

HQL 325

SEQ 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD

======

HITS AT: 141-146

REFERENCE 1: 133:318297

L3 ANSWER 29 OF 38 REGISTRY COPYRIGHT 2003 ACS

EM 302411-43-4 REGISTRY

DN Protein (Arabidopsis thaliana clone Ceres 2113368) (9CI) (CA INDEX NAME)

DTHER NAMES:

MN 163: PN: EP1033405 SEQID: 55163 claimed protein.

FQL 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS

======

HITS AT: 72-77

F.EFEF.ENCE 1: 133:318296

L3 ANSWER 30 OF 38 REGISTRY COPYRIGHT 2003 ACS

FM 302411-42-3 REGISTRY

The Protein (Arabidopsis thaliana clone Ceres 2113367) (9CI) (CA INDEX NAME)

DTHER NAMES:

N 162: PN: EP1033405 SEQID: 55162 claimed protein

:QL 325

JEQ 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD

======

HITS AT: 141-146

FHFERENCE 1: 133:318296

13 AMSWER 31 OF 38 REGISTRY COPYRIGHT 2003 ACS

EN 301564-27-2 REGISTRY

CN - Protein (Arabidopsis thaliana clone Ceres 1025180) (9CI) (CA INDEX MAME)

OTHER NAMES:

CM 1596: PN: EP1033405 SEQID: 7409 claimed protein

3QL 256

DEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS

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HITS AT: 72-77

REFERENCE 1: 133:306360

L3 ANSWER 32 OF 38 REGISTRY COFYRIGHT 2003 HOS

RM 301564-06-1 REGISTRY

(N) Protein Arabidopsis thaliana block Caras 19861780 AND CA INDEX MAKE

THER TAMES:

(N) 1898: PM: E81033408 SEQUE: 0408 Slaimed Systems.

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MaRkithky 19 912414

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1.1. ACCUT METME ROAPTITUTO A GELIKOTRATI TESPYTTITI MARMHEEWIL
 HITS AT: 141-146
 **RELATED SEGMENORS AVAILABLE WITH SEGMENT.
REFERENCE 1: 133:306361
 <u>. 3</u>
           AMSWER 33 OF 38 BERINDER OFFREHED 1918 AND
            286839-23-4 PRGISTRY
 H.1.
               I-Phenylalanine, I-tryytogogl-l-valy.-i-alany.-i-tryytogog.-i-n.wtray.-
                                  ON THEE MAKE
 OTHER NAMES:
 CM | 13: FM: Wolld44771 SEQID: We unclaimed wequence
 SQL
            To the same of the
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                              ===----
HITTO AT:
REFERENCE 1: 133:145915
          ANSWER 34 OF 38 REGISTRY COPYRIGHT 2003 ACS
L3
             286839-22-3 REGISTRY
RN
             1-Phenylalanine, 1-tryptophyl-1-alanyl-1-arginyl-1-tryptophyl-1-histidyl-
                                  (CA INDEX MAME
CN 12: PN: W00044771 SEQID: 21 unclaimed sequence
SQL
            1 WARWHF
SEQ
                             ==::::::::=
HITS AT:
                             1-6
REFERENCE 1: 193:148918
1.3
          ANSWER 35 OF 38 REGISTRY COPYRIGHT 2003 ACS
            286839-16-5 REGISTRY
RN
             L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-tryptophyl-L-histidyl-
(901) <sup>1</sup> (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: W00044771 SEQID: 2 claimed sequence
SQL
            1 WEARE
SEC
                             \hat{1} = \hat{\phi}
HITS AT:
REFERENCE 1: 133:145915
L3
           ANSWER 36 OF 38 REGISTRY COPYRIGHT 2003 ACS
            Protein Byllin Myrobana lum tubernu ole ere en En ere en ere ere
OTHER NAMES:
          - GenBank Allili419-derived protein di Usismie
                        1 MITRIMERSS FURROSHIPR AREHIVIUME ETHAPULF H. ITAGELIANS
SEÇ
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 $H : T : \mathcal{A} : \mathbb{R} \to \mathbb{R}$

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**RELATED SEQUENCES AVAILABLE WITH SEQUENCES

REFERENCE 1: 180:120305

BEFFFFILE : 1. HILLS

ANSWER STOR SER REGINTER OFFERIGHT LOSS AND 2042TP-11-1 RESISTEM

EX

Desaturase, fatty acid .cmega.6- (Chlamydomonas reinhardsii blone pCDI gene des6 reduped) (GCI) (CA INDEM NAME)

OTHER NAMES:

..omega.@ Desaturase - Thlamydomonas reinhardtii -lune pCD1 pene des@ 2 - 3223-3

GenBank Ab. Tw4 -derive: ristein 31 swhemin

SQL

SEQ 201 VTEADMAKWD STSAMLYKVF LGTPLKEWAS VGHWLVWHFD ENKYTPKORT

HITS AT: 234-239

REFERENCE 1: 128:21493"

L3 ANSWER 38 OF 38 REGISTRY COFFRIGHT ALLS ADD

RN 171885-85-1 REGISTRY

CN Protein TraH (plasmid pMEA3001 [901] 10A INDEM NAME

OTHER MAMES:

CN Protein TraH (Amyoclatopsis methanolica plasmid pMEA300)

SEQ 1 MFTPEPKPTT DHTGQSTTEA VEARRAADLA LYTNAKYPTR TTOTVSWIGW

51 HEGELSGYVV PLGLGARYWD GEYALSLETA LGWAANELRE RRQQRAYRTR

HITS AT: 47-52

REFERENCE 1: 124:47157

=> fil hoaplus FILE 'HOAFLOO' ENTERED AT 13:57:58 ON 13 FEE 2003 USE IS SUBJECT TO THE TERMS OF YOUR SIX CUSTOMER AGREEMENT. PLEASE SEE "HELF TRABETERMS" FOR DETAILS.
ODFYFIGHT OF DETAILS. Oppyright of the artifles to which records in this database refer is held by the publishers listed in the FUBLISHER. FB. field [available] for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications. The CA Lexison is the copyrighted intellectual property of the the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, oppoint, or strong of this internation, without the prior well-ten or meant of Wal, is strictly prohibites. FILE COMERS 1907 - 13 Feb 2003 | TOL 139 188 T FILE LAST MEDATED: 12 Feb 2003 | (2003)210/ED; This file contains CAS Registry Numbers for easy and accurate substance identification. = $[\cdot]$ ==: d stat que 115 1 SEA FILE=REGISTRY ABB=ON PLU=ON WVRWHF/SQSP 1110 SEA FILE=REGISTRY ABB=ON PLU=ON W[GAILVSTKRHF] [GAILVSTKRHF]W[LĹ GAILVSTKRHF]F/SQSF 36 SEA FILE=REGISTRY ABB=ON FILM=ON WOLWAILUSTRO GAILUSTROWHF/SOCK 1 SEA FILE=HOAPLUS ABB=ON PLU=ON L1
20 SEA FILE=HOAPLUS ABB=ON PLU=ON L5
1 SEA FILE=HOAPLUS ABB=ON PLU=ON L5 AND L6
19 SEA FILE=REGISTRY ABB=ON PLU=ON L12 AND SQL=<50
53 SEA FILE=HOAPLUS ABB=ON FLU=ON L12
18 SEA FILE=HOAPLUS ABB=ON PLU=ON L13 MOT (2003 OR 2012)/FY
17 SEA FILE=HOAPLUS ABB=ON PLU=ON L14 NOT (L6 OR LT) L5 = ~ =) · => d ibib abs hittm 115 1-17 L15 ANSWER 1 OF 17 HCAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 2002:36295 HCAFLUS DOCUMENT NUMBER: TITLE: 137:1818 Murleir arids and their enried polypeptides in a human tissues Tang, Y. Tom, Liu, Thenghra, Ormanac, Radoje T. Hyseg, Inc., USA INVENTOR(S): PATENT ASSIGNEE (8): SOURCE: FOT Tht. Appl., 147 CLOEN: FIRMI 11.

DOCUMENT THEE: LANGUAGE: Fn. :118h FAMILI ASS. NO. 1111:

PATENT INFORMATION:

PATERT NO. MANN TATE

F 4-10-

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BRICHITY APPLN. INFO.:
     The present invention provides a collection or library of 13,901 nucleic
     adid conting sequences assembled from empressed sequence tag or cDNA
     libraries isolated mainly by sequencing by hybridization (SBH), std. PCR,
     Sanger sequencing techniques, and in some cases, sequences obtained from one or more public databases. The oDMA libraries are from human tissue
     sources and hearest heighbor sequence homologies are provided. The
     invention also relates to the proteins encoded by such polynuclectides,
     along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. (This abstr. record is the fourth of four
     records for this document necessitated by the large no. of index entries
     required to fully index the document and tublication system constraints. ..
IT
     432700-32-8
     RL: ANT (Analyte); BSU (Biological study, unclassified); PBE Proporties;
     THO Otherspeufin use ; Anno Ansiminal known; Fill Ball a sale in any ;
        (amino acid sequence; nucleic acids and their encoded polypeptides from
        human tissues)
L15 ANSWER 2 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:898070 HCAPLUS DOCUMENT NUMBER: 137:16818
                          Human polypeptide fragments and their encoding cDNA
                          - polynuoleitides
INVENTOR 3: Shinkets, Richard A.; Leach, Martin D. PATENT ASSIGNEE(S): Curagen Corporation, USA SOURCE: PCT Int. Appl., 1037 pp.
                          CODEN: FIXXD2
DOCUMENT TYPE:
                          Patent
LANGUAGE:
                           English
FAMILY ACC. NUM. COUNT: 8
PATENT INFORMATION:
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DE, DK, ES, F1, FF, GB, GK, IE, IT, LU, MY, ML, FT, SE, TR, BF, EJ, CF, CG, C1, CM, GA, CN, GW, ML, MB, NE, SN, TD, TG
                                                 FRICHITY APPLN. INFO.:
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The present invention provides 11,491 ORFM, hovel human polypeptide fragments, as well as the 11,491 DDNA fragments encoding ORFM and antibodies that immunispecifically bind to ORFM or any derivs., variants, mutants, or fragments of the ORFM polypeptides, polynucleotides, or antibodies. The invention addnl. provides methods in which the ORFM polypeptides, polynupleotides, and antibodies are used in detection and treatment of a broad range of pathol. States, as well as to their uses. [This about, result is one of live reserving to the large no. of index entries required to facily in extens a constant and publication system constraints.].

IT 434378-63-9P

CORPORATE SOURCE:

RL: ANT (Analyte); BFN 'Bicsynthetic greparation'; BSU (Biological study, unclassified); FRP (Properties); THO (Therapeutic use); ANST (Analytical study); BTOL (Biological study); FREF (Freparation); DSES (Uses) (amino acid sequence; human polyperhide tragments and their encoding pDNA polymuslectides)

L15 ANSWER 3 OF 17 HOAPLUS COPYRIGHT 2003 ACS 2000:273192 HCAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 133:295042

TITLE: Selection of an immunogenic and protective epitope of

the PsaA protein of Streptococcus pneumoniae using a

phage display library

AJTHOR(S):Srivastava, N.; Zeiler, J. L.; Smithson, S. L.;

Carlone, G. M.; Adws, E. W.; Sampson, J. S.; Johnson,

S. E.; Kieber-Emmons, T.; Westerlink, M. A. J. Department of Medicine, Medical College of Ohio,

Toledo, OH, 43614, USA

Hybridoma (2000), 19(1), 23-31 CODEN: HYBRDY; ISSN: 0272-457M SOURCE:

PUBLISHER: Mary Ann Liebert, Inc.

DOCUMENT TYPE: 'ournal LANGTAGE: English

AB Streptocopous pheumoniae in an important path genotiat crasses inserate in young and elderly individuals. The currently available polysaccharide vaccines have limited efficacy in those age groups most susceptible to pneumococcal infections. This study focuses on mapping the epitopes of a surface protein of S. pneumoniae by biopanning a 15 mer phage display library using 5 different monoplonal antibodies (MADs) against the Pheumoccal surface adhesin A (PsaA). PsaA is a component of the bacterial dell wall that is highly species specific and is involved in bacterial adherence and virulence. Biopanning of the phage display library reveals three distinct epitopes on the PsaA protein. The sequence homol, of these epitopes ranges from two to six amino acids when compared to the native FsaA protein type 2. Two of these epitopes have been evaluated for their immunogenicity in mice. The peptide selected by the MAbs 8G12, 6F6, and 18" is referred to as the consensus peptide and is immunogenic in mide. Optimal anti-PsaA response is obsd. in mice immunized with 5 \ .mu. s of the consensus peptide complexed to proteosomes in 1:1 ratio. The anti-PsaA consensus peptide complexed to proteosomes in 1:1 rapie. The anti-PsaA response is significantly I were than the response to the IsaA native protein. The peptide of least high many many many and the following in form is similificantly protest, we have a many many and the protein. These serotype a when compared to mise immunised with the native protein. These results show that the selected epitopes are its least protein are immunipanit and protective in mise. These epitopes need to be evaluated further as alternatives to currently available varsines.

301300-56-1

Pl: FA: Fitligibal activity or effect., embept aiverse ; FAU Fitligibal study, unclassified ; THU Therapeutic use; FIDL Bitligibal study; USES (Uses)

'PsaA protein of Streptocolous pheumlhiae in vaccine adainst

streptinional infections
REFERENCE COUNT: 64 TI THERE ARE MAINLESS REFERENCES ANALYARISE E E LEIS BECALL AND CHAIL DO ROWLLESS IN 186 FF F REEL

L18 ANSWER 4 FF 17 HOAFDMS THEFFICED TO A M 199::077.07 BrARION 131:198616 ACCESSION NUMBER:
DOCUMENT NUMBER:
DITLE:

Epitope peptides immunojenio against Streptomodous

pheumoniae and their use in vaccines

INVENTOR(S): Carlone, George M.; Ades, Edwin W.; Sampson, Jacquelyn

S.; Tharpe, Jean A.; Zeiler, Joan Louise; Westerink, Maria Anna Julia

The Government of the United States of America, Represented by the Secretary, USA FATENT ASSIGNEE D.:

FOT Int. Appll, 59 pp. CODEN: PIXXD2 SOURCE:

DOGUMENT TYPE: Fatent LANGUAGE: English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

FAT	ENT	NO.		KI:	111	CATE			is -		Mil			LATE			
WO	9945	121		Ā	_	1999	 3913		1.1	3 19	99-0	 8452	 3	1999	 		
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		DK,	ΞΞ,	ΞS,	ΞΞ,	GB,	GD,	GΞ,	G∺,	3,	HR,	HT,	Ŧ D,		T.N.,	IS,	J₽,
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		ТJ,													•	•	·
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									LU,								
									ΝE,								
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	9927													1999	0226		
BR	9908	476		A		200C	1205		В	R 19	99-8	476		1999	0226		
EF	1060.	249		A	-	2000	1220		E	F 19	99-9	0854	3	1999	0226		
	R:	AT,	ΒE,	CH,	DE,	DK,	ES,	FR,	GB,	GR,	- m	LI,	LU,	NL,	SE,	MC,	PT,
		ΞĒ,	ΞI							·	·	·		·	·	·	·
171	REF		INFO	. :					US 1:	223-1	7656.	3 F	E	1995	1302		

FRICE

WO 1999-US4326 W 19990226

Peptides are provided which immunospecifically bind to monoclonal ΞÆ antibodies specific for the 37-kDa pneumococcal surface adhesion A protein (PsaA) of Streptococcus pneumoniae of the invention, and that are immunogenio against Strepthochous pheumoniae infermion. Also provided are vaccines comprising such immunityering polypeptides, and methods of conferring protective immunity against Offert consequencing protective immunity against Offert schools promonies infection by administering therapeutic ompose comprising the immunity reptides of the invention. Also provided are methods of detecting the presence of Streptococcus pneumoniae in a sample using antibodies or antigens, and methods of preventing and treating Streptococcus pneumoniae infection in a subject. In addn. a phage display method of identifying the sequence of a peptide potentially rapable of eliciting protective immunity against a pathogenic microerganism is provided.

241814-51-7P

FL: BEN Bi synthetic pregaration ; FBF Properties ; THY Therapeutic use; EICL Biological study; FBEF Preparation ; USES Uses: (epitope peptides immunogenio adainst Streptodorous pneumoniae and their use in vaccines

THERE ARE & COTEC REFERENCES AVAILABLE FOR TELS REFERENCE COUNT: 8 PETTRO. AND STREETING AVAILABLE IN THE RE FORMAT

LIB ANSWER ROOF IN HOAFLUS CORPRIGHT 2005 ACS ACCESSION NUMBER: 1998:485741 HOAFLTO

129:76469

Heparin- and sulfatide-binding peptides from the type I repeats of human thrombospondin and conjugates

thereof for treatment of metastatic tumors and other necessularization-related diseases

Roberts, Tavid D.; Browning, Phillip J.; Bryant, Joseph INTENTOR'S :

L.; Inman, John R.; Mrutosch, Henry C.; Gul, Nenghua United States Dept. of Health and Human Jervices, USA

FATENT ASSIGNEE (S): SOURCE: U.S., 133 pp., Cont.-in-part of U.S. 215,095,

abandoned.

CODEN: TURMAM

DOCUMENT TYPE: Patent LANGUAGE: English

FAMILY ACC. NUM. COUNT: PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO. DATE
US 5770563 US 801812 US 8357041		19980623 19921215 19941018	US 1995-487568 19950607 US 1991-801812 19911206
US 6051549 PRIORITY APPLN. INFO	A O.:	20000418	US 1998-41119 19980311 US 1991-801812 A2 19911206 US 1994-215085 B2 19940321
			US 1995-487568 A1 19950607

OTHER SOURCE(S): MARFAT 129:76489

AB This invention identifies a biol. active group of peptide sequences from Type I repeat units of the extracellular matrix protein, human thrombospondin-1, identical or homologous to the sequence, KRFKQDGGWSHWSPWSSC (SEQ ID NO:30). The biol. activities residing with the full sequences, portions thereof, and variants of the full or partial sequences are displaced. The inventor mesorible of which is a control of be contained by devalently linking these particles to a classe transfers, preferably a branched, water-sol, polymer of low or absently which the immunogenicity, such as polysucrose (Figoll). The invention describes (1) a method for prepg. such conjugates, (2) the use of the defined peptides or their conjugates in blocking or modifying the action on cellular processes of heparin (e.g., proliferation, adhesion, motility, extravasation and neovasbularidation', sulfatides, related sulfated glycoconfugates, dibronectin, and basis dibroblast drowth factor, involving malignant cell lines and normal endothelial cells. The of the defined peptides, analogs or peptidomimetics and their conjugates for treatment of metastatic tumors, breast carcinomas, melanomas, Kaposi's sarcomas, hemandiomas, diabetic retinopathies, and various pathol. conditions dependent upon neovascularization is also disclosed.

209457-55-6

RL: BAC (Biological activity or effector, except adverse); BFR (Biological process); BSC (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); FIOL (Biological study); FROC (Frecess); USES (Uses) (heparin- and sulfatile-binding perilos from the type I reports of human thrombospondin and conjudates thereof for treatment of merastatic tumers and other necrasorialization-related discusses

REFERENCE COUNT: 28 THESE ARE 18 CITED SEPERENCES AVAILABLE FOR THIS SECUED. ALL COLATIONS AVAILABLE IN THE SE FORMAT

Lie Amswer C of IT HEARINS CHERRISHT CON ACC ACCESSION NUMBER: 1999: CARREST HEARING CONTENT NUMBER: 129: Fire

Fau- 51

M-Relver 13 212414

TITLE: A region from the medium chain adaptor subunit (.mu.) recignities leutine- and tyrosine-based sorting signals Brennes, Tobil; Lautrak, Viadis; Lindavist, Bitch; AUTHUR 31: Bakke, didmuni COMPORATE SOMECE: Dep. Milesular Cell Bl 1., fibial mobile by, Thib. iv., p. 1910, p. 916, it stray
Sturnel of blood value Themletsy of two, p. 1901, p.
800me644 STIBLE: donem: Jereas, Isam: 0 21-9206 American Society for Bilchemistry and Molecular PTELISHEF: Bislogy DOCUMENT TYPE: Journal LANGUAGE: English Tyrosine-based sorting signals in the sytosolic tails of membrane proteins have been found to bind directly to the medium chain subunit (.mu.) of the adaptor complexes AF-1 and AF-2. For the leucine-based signals, an AB. interaction with AF-1 and AF-2 has been reported, but no specific interacting subunit has been demonstrated. After searching for mols. interacting with the leucine-based sorting signals within the cytosolic tail of the major histocompatibility complex class II-assocd. invariant chain using a phage display approach, we identified phage clones with homol, to a conserved region of the AF-1 and AP-2 .mu. chains. To investigate the relevance of these findings, we have expressed regions of mouse .mu.1 and .mu.2 chains on phage gene product III and investigated the binding to tail sequences from various transmembrane proteins with known endosomal targeting signals. Enzyme-linked immunosorbent binding assays showed that these phages specifically recognized pectides contg. functional leudine- and tyrosine-based sorting signals, suggesting that these regions of the .mu.l and .mu.2 chains interact with both types of sorting signals. 208192-30-7P RL: BPN (Biosynthetic preparation,; Elk (Biological process); BST (Biological study, unclassified); BIOL (Biological study); FREP (Freparation); PROC (Frocess) (region from medium chain adaptor subunit (.mu.) of AP-1 and AF-2 recognizes leucine- and tyrosine-based sorting signals) 44 THÊRE ARE 44 CITED REFÉRENCES AVAILABLE FOR THIS REFERENCE COUNT: RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT LIS ANSWER 7 OF 17 HOAFLUS COPYRIGHT 2013 AGS 1998:11596 HCAPLUS ACCESSION NUMBER: DOCUMENT NUMBER: 129:110913 Amino acids within residues 181-200 of the nicotinic TITLE: acetylcholine receptor .alpha.1 subunit involved in nicetine binding AUTHOR(S): Lentz, Thomas L.; Chaturredi, Vilaya; Conti-Fine, Bianda M. Department of Cell Birl by, Yale University Coh. 1 or Well risk, New Haren, 71, - - , 757 Birchemical Hearnagely by John , 17 by, 541-547 CORPORATE SOURCE: SOURCE: -001FM: FoFORe; ISOM: 1:16-Lend Elsevier Science Inc. PUBLISHER: DOCUMENT TYPE: Journal LANGUAGE: English AB Structural determinants of L-[3H]nicotine binding to the sequence flanking Cys 190 and Cys 193 of the Torpedo abetyloholine receptor .alpha.1 subunit were investible in since synthetic pertides cresibles 191-200 and fusion proteins crossines 100-31. was compared with "I paytides and fusion proteins in which individual amin. A dide at positions lelevely were substituted. Substitution of Lys let, Tyr 190, Tys 182, Cys 193, Thr 196, and Tyr 198 resulted in the greatest redn. in his time binding. Equil. binding of [3H] misotime to pentide [:1-u]) revealed a binding component with an apparent KD of 1.2

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.mu.M. Johatlation of Lya law with Aug, Hooler, Lyr Lau, Tya 180, Tya
193, and Tyr 198 resultablin a significant radn. In affinity. Affinity
      was not affected significantly by substitution of Arg 182, Lys 185 (with
      Sly or Arg., Val 188, Tyr 189, Pro 184, Asp 188, Thr 196, and Asp 200. It is concluded that Lys 188, His 188, Tyr 191, Tys 192, Cys 189, and Tyr 198 play the meatest role in nicotine binding to residues 191-20 of the salphall substitute Fred La studies have implicated Tyr 18, Cys 182, Cys
       led, and Tyr 198 in america binding to the aboughdedline reservior. These
      results of hims a rule for these residues and also demonstrate a function for Lys 1-6 and His 166 in hipotine binding.
      201529-09-1
      RL: BPR (Biological probess); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Probess)
          [181-200] midotimic receptor .alpha.1-subunit mutant; misotimid
          adetylyholine redeptor lalpha.1 subunit residues 181-270 in hidotine
         binding)
LIS ANSWER 8 OF IT HOARDING COPYRIGHT DES
ACCESSION NUMBER: 1090:53391 HEARDIS
DOCUMENT NUMBER: 124:114958
ACCESSION NUMBER:
TITLE:
                              Isolation and characterization of antibodies which
                              specifically recognize the peptide encoded by exon 7
                              (v2) of the human CD44 gene
AUTHOR(S):
                              Borgya, A; Woodman, A; Sugiyama, M; Donie, F;
                              Kopetoki, E.; Matsumura, Y; Tarin, D
                              Puchringer Mannheim SmbH, Fennberg, D-81971, Germany Clinical McLecular Pathology (1995), 48(5), M241-M250 CODEN: CMPAFI; ISSN: 1355-2910 BMJ Publishing Group
CORFORATE SOURCE:
SOURCE:
FUBLISHER:
DOCUMENT TYPE:
                              Journal
LANGUAGE:
                              English
    Exon 7 of the human CD44 gene is overexpressed in many commonly occurring
     carcinomas. The aim of the study was to explore the diagnostic and
     therapeutic potential of this frequent abnormality. A new mencelonal
     antibody (mAb, M-23.6.1) and a polyplonal antibody (pAb, S-6127) to the
     corresponding antigen were raised by immuniting mide and sheep, resp.,
     with a specially constructed fusion protein HIV2 (gp32)-CD44 exon 1
     Characterization of mAb M-23.6.1 by ELISA, Western blotting,
     immunocytochem., and FACS anal. confirmed that it specifically recognizes
     an epitope in the region between amino abids 19 and 33 of the poptide
     encoded by this exon. Western blotting expts. With two cell lines, RT111
     and ZR75-1, known from RT-FCR data to be over-transcribing the emon,
     yielded a monospecific band of approx. All kDa, and immunocytochem. showed
     discrete membrane staining on the same cell lines. Fluorescent antibody
     cell sorting (FACS) revealed binding to greater than 90% of the cells of
     each of these lines. Specificity of recognition of the antigen was shown
     by inhibition of the precise immunoreactivity typically seen in ELISA and
     Western blots, by pre-incubation with synthetic exon 7 peptide or
     fragments of it. The new antibodies will be useful tools for the further
     anal. of abnormal CD44 isoforms and their plin. implications.
     172997-35-2
     RL: BPR (Biological process'; BSU (Biological study, unclassified); BIOL
      (Biological study); FBWC (Frodess)
         (isolation and characterization of monoplonal antibody to peptide
         encoded by exam 7 of human CD44
LIS AMSMER 9 OF 17 HOAFLUS COPYRIGHT 1113 ACS
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LIS ANSWER 9 OF 10 HOAFLUS COPYRIGHT 1003 ACS

ACCESSION NUMBER: 1880:980102 HOAFLUS

DOCUMENT NUMBER: 113:380019

TITLE: Two subsites in the binding brack of the incidence of
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Fuchs, Sara
 MORFHRATE SKUPME:
                                                          Chemidal Immunology, Weimmann Inst. Science,
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Frozeedings of the National Academy of Unionies of the
United States of America 1920, Al 18 , 178 1-8
CODEM: PMASA6, ISSN: [027-8424
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                                               National Adadens of Adenses
: TELLINE:
I DOUMENT TYPE:
                                                 Journal
 LANGTAGE:
                                               English
         The ligand binding with of the him tining abstylenguine receptor. As in Fisher ligand binding with of the him tining abstylenguine the random of spalited in the calpha. He would within a specific order of the factor of the calphana to be an approximately as a part of the factor of the calphana to be a specific order.
         animal species that are resistant to lalpha. - neurotoxins, the authors have
         previously shown that for residues in this region, at positions 187, 189,
          194, and 197, differ between animals sensitive 'e.g., mouse) and resistant
          (e.g., mongoose and snake) to .alpha.-bungarotomin (.alpha.-BTM). In the
         present study, the authors performed site-directed mutagenesis on a
          fragment of the mongoose AcCheR .alpha.-subunit (residues 122-205) and
         exchanged residues 187, 189, 194, and 197, either alone or in combination,
         with those present in the mouse .alpha.-subunit sequence. Only the
         mangabase fragmant in which all four residues were mutated to the mouse
         ones exhibited .alpha.-BTX binding similar to that of the mouse fragment.
         The mongoose double mutation in which Leu-194 and His-197 were replaced
         with proline residues, which are present at these positions in the mouse
         AcchoR and in all other toxin binders, bound .alpha.-BTX to .apprxeq.60%
         of the level of binding exhibited by the mouse fragment. In addn., replacement of either Pro-194 or -197 in the mouse fragment with serine
         and histidine, resp., markedly decreased .alpha.-PTW kinding. All other mutations resulted in no or just a small introduction. Subject the first propose two subsites in the kinding domain for .alpha.-BTW: the proline subsite, which includes Pro-194 and
         -197 and is crit. for .alpha.-BTX binding, and the arom. subsite, which
         includes amino acid residues 187 and 189 and dets. the extent of
         .alpha.-BTX binding.
         170662-94-9, EARGWKHWVFYACCLTTHYLD 170662-98-3,
         EARGWKHWYFYACOFTTHYLD 170662-99-4, EARGWKHWYFYACOLTTFYLD
         170663-00-0, EARGWKHWVFYACCPTTPYLD
         FL: BPR (Birlomical process); ESU (Biological study, unclassified); FRF
         (Fromerties); BIOL (Biological study); PROC (Process)
                (mongoose nicotinic receptor .alpha.-subunit binding domain mutant
               centg.; nicetinic receptor .alpha.-subunit .alpha.-bungaretexin-binding
               domain arom. subsite and proline subsite)
         170663-01-1, EARGWKHWVFYSCOPTTPYLD
         RL: BFR (Biological process); BSU (Biological study, unclassified); FRP
         (Properties); BIOL (Biological study); FROC (Process)
                mouse nicotinio receptor .alphal-subunit kinding domain conta.;
               nicctinic receptor .alpha.-subunit .alpha.-bungarot win-sindong domain
               arcm. subsite and proline subsite'
         170663-02-2, EARGMKHWVFYSCWPTTPYLD 170663-03-3,
         EARGWKHWUFYSCOSTTPYLD 170663-04-4, EARGWKHWUFYSCOPTTHYLL
         RL: BFR (Piological process); BST (Biological study, unclassified); FBF
          Reporting ( COST ; The strip of the control of the second strip of
               (mouse nicotinic receptor .alpha.-subunit binding domain mutant contg.;
               nicetinie receptor .alpha.-subunit .alpha.-bun marctowin-binding domain
              arim. Subsite and proline subsite
LIS ANSWER IN OF IT HOAPLI'S COEYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:703749 HOAPLI'S
COCKENT NUMBER: 121:203099
TITLE:
                                              Profile of the regions of abetyloholine reportor
                                               Lalpha, chain recognised by T-lymphocytes and by
                                               antibodies in HAMS-susceptible and non-susceptible
                                               mouse strains after different periods of immunication
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50 90 CHAP - F RO 414 with the reput of Al D. 147 (1976) Oshima, Minako, Pachher, Andrew R., Atasei, M. Gouhair AUTHORIE: CORPORATE SOURCE: Dem. Biochem., Baylor Coll. Med., Houston, TM, PHIERE: Male malas Immostlagy (1994), 31 11 , 493-43 outen: Moimot, isoùî oitie et 131131313131 English AB | 08781/6 (86) mide develop a neuromusqular disease, emptl. autoimmune myasthemia gravis (EAMG), after .gtoreq.2 immunizations with Torpedo baliforniza abetylpholine receptor (AChR). To det. whether EAMG is related to recognition of particular region(s) on the main extracellular domain of the .alpha. chain (residues .alpha. 1-210) in prolonged

immunication, the authors have examd, the differences in the antibody and T rell resignition provides of Bo and CVL a obtain that ites not develop EAMG) mide after different periods and a no. of immunication with Torpedo AChR. In a given strain, antibodies and T cells recognized immunodominant regions, which may coincide or may be uniquely B cell or T cell determinants. Both B6 and SJL exhibited similar antibody recognition profiles after the 2nd and through the 4th immunitations with ATER. Major profiles after the 2nd and through the 4th immunications with AlnB. Mail's differences between the 2 strains were a und in their Totall remainablish of regions in the second part (residues 1.1-1.1), or the main extracellular domain of the Lalpha, chain. Totalls at SIL recognized consistently only one region (111-126) within this part of the Lalpha, chain, whereas in E6, Totall recognition of 3 peptides (111-126, 146-162, and 182-198) and next neighbor regions to them persisted throughout the period. Of these 3 pertides, 146-162 was an immunodominant pertide unique to B6, as the other 2 pertides (111-126 and 132-198) were also recognized by either T cells or antibodies in SJL. To study the role of T cells recognizing region 146-162 in EAMG, a T cell line was generated against this region and the cells transferred into B6 mice followed by one Torpedo AChR injection. Enhancement of antibody prodn. toward .alpha. chain peptides was obsd. as an influence of T cell transfer compared to profiles at 1 wk. In addn., 1 out of 3 mice examd. showed signs of EAMS. These results suggest the importance of T cells recognizing residues 146-162 in EAMG. Thus, the presence of persistent T cell responses to the second half (residues 100-210) of the main extracellular domain of the .alpha. chain is assocd. with the development of EAMG in B6 mice, while absence of these responses in SJL mice may enable them to escape the disease. The preservation of the immunodominance of peptide 146-162 in the local reconstruction of being probably most important for the pathogenesis of FAMA in this obtain.

157960-63-9

RL: BIOL (Biological study)

(in B- and T-cell epitope mapping on acetylcholine receptor .alpha. chain, autoimmune myasthenia gravis in relation to;

LIS ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS 1994:318925 HCAPLUS ACCESSION NUMBER:

12::31880° Diagnosis of tumors by assay of CD44 splicing patterns

Tarin, David; Matsumura, Yasuhiro

FATENT ASSIGNEE(S): ISIS Innevation Ltd., UK PCT Int. Appl., 41 pp. SOURCE:

GODEN: FIXXD2

DOCUMENT TYPE: Patent LANGUAGE: Enalish FAMILY ACC. NOW. COUNT:

PATENT INFORMATION:

PATENT NO. HIND DATE EFFILINGIAN . INTE _____ ____ _____ WI 9412F33 AI 1 + 14 1 ... 1 TWO 1923-0816UT - 19931TU W: 3A, M, 98

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BW: AC, BE, MH, CE, CF, ES, FR, MH, MH, CH, CT, CM, MM, ML, FT, SE
RE1820 AC 19980817 EF 1993-916109 19930720
851822 B1 19960417
     EP 661620
         AT 1:485-91919
W1 1:485-38, 931
        136940
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19347878
         7: 7A,
                      EX: AT, BE,
     CA 2149639
EP 672130
                      AT TWENSE BY 1947 240 TW MILES
CH, DH, DK, ES, PR, SH, GR, TR, TT, BI, DV, MC, ML, PT, SH
A 19981115 US 1998-873284 19980417
A 19940319 US 1998-428186 18988817
         R: AT, BE,
        5931646
     US 8579898
PRIORITY APPLN. INFO.:
                                           3B 1992-15494
                                                                1402112
                                           38 1992-0434v
                                           .
38 1992-20105
                                          WO 1993-GB1520
                                                               19930720
                                          WD 1993-GB2394
                                                              19931122
     There is marked over-expression of multiple spliced variants of the CD44
     gene in tumor compared to counterpart normal tissue. This observation
     forms the basis of a method of diagnosing neoplasia by anal. of a sample
     of body tissue or body fluid or waste product. A new exon 6, of 129 bp,
     has been found and sequenced, and is claimed as such and for use in the
     diagnostic method. Samples of breast tumors were assayed for 0044 mRMA by
     reverse transcription/PCR using primers to detect hemopoletic CD44
     followed by hybridization with a probe from exon 4. A no. of splice
     variants were found in neoplastic tissue that were absent from normal
     tissue, this was found in all patients tested. There was a difference in
     splice patterns between neoplastic and non-neoplastic diseased tissues
     (cystic disease). Similar results were found in colon cancer using biopsy
     and stool samples and in bladder cancer using urine samples for diagnosis.
     155216-25-4
     RL: PRP 'Properties
        (amino acid sequence of, in neoplastic tissue, altered splining
        patterns in neoplastic tissue in relation to)
L15 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS
                       1992:564026 HCAPLUS
ACCESSION NUMBER:
DOCUMENT NUMBER:
                          117:164026
TITLE:
                          Species- and subtype-specific recognition by antibody
                          WF6 of a sequence segment forming an
                          .alpha.-bungaretewin binding site on the midetinic
                          acetylcholine receptor .alpha. subunit
AUTHOR(S):
                          Molane, M. E.; Fritzen, M.; Wu, M.; Diethelm, B.;
                          Maelicke, A.; Conti-Tronconi, B. M.
                          Coll. Biol. Sci., Univ. Minnesota, St. Paul, MN,
CORPORATE SOURCE:
                          55108, USA
                           Journal of Redeptor Basearth (1980), 12 3 , 199-421
CODEM: TERROW, 1980: 1884-111
SOURCE:
DOCUMENT TYPE:
LAMGTAGE:
     The monoclonal antibody WFC computes with acceptions one and
     .alpha.-bungarotoxin (lalpha.-BBT) for binding to the Torpedo nicotinic
     acetylcholine rwdeptor (nAChR) .alpha.1 subunit. By using synthetic
     peptides corresponding to the complete Torpedo nAChR .alpha.1 subunit, the
     authors previously mapped a continuous epitope recommized by WFG, and the prototope for Lalpha.-BGT, to the sequence segment Lalpha.1,181-2100.
     Single aming avid substitution analysis have been used as an initial
     approach to details on it. aming and is for WFC and Lalpha. -POT kinding.
     in the present study, the authors continue the anal. of the structural
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features of the WFE epitope by comparing its pross-reactivity with

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symphetic pertides thereopenains to the lagrant wall was mitted to the business nAThRs of different species, the ratorials adjust, capacity calputed and ralphase hathe subtypes, and the outre brain reginal-bet alma has gratein subunuts, laighal Baiter laigh all an cluaigh a Bathallaigh all an ch results indicate that WFO is able to oross-react with the muscle .alpha.l subunits of different species by virtue of conservation of several crit. amino acid ruslives between positions 197-198 of the Lalpha.1 subunit. These studies further define the essential structural features of the sequence segment .alpha.1 (181-20%) required to form the epitope for WF6.

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BL: BILL Bi logical study lantibody to nitritinit resept a bungarot, win binding site kinding by,

structure in relation to)

115 ANSWER 13 OF 17 HOAPLUS COPYRIGHT 2003 ACS ACCESSION NUMBER: 1991:223857 HCAFLUS

114:22385

DOCUMENT NUMBER: TITLE: Structural determinants of .alpha.-bungarotomin

binding to the sequence segment 181-200 of the musile

nicotinio ameryloisline as sept sollagos, oramnit: effects of systems systems books and such species-specific amino acia substitutions

McLane, Kathryn E.; Wu, Wiadong; Diethelm, Brenda; AUTHOR(S):

Conti-Tronconi, Bianca M. Coll. Biol. Sci., Univ. Minnescta, St. Paul, MN, CORPORATE SOURCE:

55108, USA

Biochemistry (1991), 30(20), 4925-34 CODEN: BICHAW; ISSN: 0006-2966 SOURCE:

DOCUMENT TYPE: Cournal LANGUAGE: English

The sequence segment 181-200 of the Torpedo nicotinic acetylcholine receptor (nAChR) .alpha. subunit forms a binding site for .alpha.-bungarotoxin (.alpha.-BTX). Synthesis peptides corresponding to the homologous sequences of human, calf, mouse, chicken, frog, and cobra muscle nAChR .alpha.1 subunits were tested for their ability to bind 125I-.alpha.-BTX, and differences in .alpha.-BTX affinity were detd. by using soln. (IC50) and a solid-phase (Kd) assays. Panels of everlapping peptides corresponding to the complete Lalpha. I subunit of mouse and human were also tested for lalpha. -BTM binding, but other sequence so ments forming the .alpha.-BTX site were not consistently detectable. The Torpedo .alpha.1(181-200) and the homologous frog and chicken peptides bound .alpha.-BTX with higher affinity (Kd .apprx. 1-2 .mu.M), ICSC .apprx. 1-2 .mu.Mo than the human and half peptides (Md .apprx. 3-5 .mu.M, ICEO .apprx. 15 .mu.M). The mouse peptide bound .alpha.-FTM weakly when attached to a solid support (Kd .apprx. 8 .mu.W) but was effective in competing for 1081-.alpha.-BTM in soln. 1081 .apprx. 1 .mu.M . The outra nAChR .alpha.1-subunit peptide did not detertably kind .alpha.-BIW in either assay. Amino acid substitutions were correlated with .alpha.-BTX binding activity of peptides from different species. The role of a putative vicinal disulfide bond between cysteine-192 and -193, relative to the Torpedo sequence, was detd. by modifying the peptides with sulfhydryl reagents. Rein, and alkylation of the peptides decreased .alpha.-BTX binding, whereas oxidn. of the peptides had little effect. Modifications of the systeine systime residues of the sobra peptide failed to induse .alpha.-PTX binding activity. Thus, while the adjacent cysteines are likely to be involved in forming the towin . Alpha. 1-subunit interface a vicinal disulfide bound was not required for .alpha. -BTW kinding.

133295-54-2P 133322-53-9P

PL: SFN (Synthetic preparation); FREP Preparation) [prepn. and .alpha.-bunnarotowin bindinaky, towin binding site of nicotinio aretylrholine receptor valpha. Adminit in relation to

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BL: SEN Syntheric preparation ; HEEF Heep matrice

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115 ANSWER 14 OF 17 HOWPLUS COFFEEDED 2003 ACS
ACCESSION NUMBER:
                               1990:525235 HCAPL
DOCUMENT NUMBER:
TITLE:
                                      113:124235
                                      Interaction of a shake wenth nearst win and a segmente
                                      fron the averyl mulline reception laipha. How mit
Bothner-By, Aksel A., Mishra, S. H., Now, Barbara W.
Dep. Chem., Carnegie Mellon Univ., Bittsburgh, BA,
ATTECR 3:
CORPORATE SUURCE:
                                     TOTA Symposia on Molecular and Cellular Fillogy, New
Series (1987), I 9 From . NOR Mol. Firl. , 19-29
CLIEB: USMELE, 1991: 10-6-74
SOURCE:
                                      Jawn.
DOCUMENT TYPE:
AB
       .alpha.-Cobratomin and adetylonoline receptor .a.pha.-subunit
       complementary binding demain populde Tresidues 179-191; were studied by 1-D and 2-D NMR spectroscopy. A model for binding is proposed.
       114753-46-7
       RL: BIOL (Biological study)
            .airha.-cobratexin binding by, conformation in, NMR study of)
LIS AMSWER 15 OF 17 HOAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                               1988:500189 HCAFLUS
DOCUMENT NUMBER:
                                      109:106189
TITLE:
                                     Binding of .alpha.-bungarotoxin to synthetic peptides
                                     corresponding to residues 173-204 of the .alpha.
                                     subunit of Torpedo, calf, and human acetylcholine
                                     receptor and restoration of high-affinity binding by
                                     sodium dodecyl sulfate
AUTHOR(S):
                                     Wilson, Paul T.; Lentz, Thomas I.
                                    Sub. Med., Yalk Thirt, them Haten, To, Te 1 , The Bischemistry of med., 2001; . ecc. -04 CODEN: BICHAM; ISSN: 0116-1261
CORPORATE SOURCE:
SOURCE:
DOCUMENT TYPE:
                                     Journal
LANGUAGE:
                                     English
       To investigate structure-function relations of a segment of the
      acetylcholine receptor .alpha. subunit, binding of .alpha.-bungarotomin to synthetic peptides corresponding to residues 173-204 of Torpedo, calf, and human .alpha. subunits was compared using a solid-phase radioassay. The
       afrinitles of 1281-labeled .alpha.-bungarotomin for the calf and human peptides were 15- and 180-fold less, resp., than for the Torpedo peptide.
       On the basis of nonconservative substitutions in the calf and human sequences, arcm. residues (Tyr-181, Trp-187, and Tyr-189) are important
       for the higher affinity binding of the Torpedo peptide. Substitution of
      neg, charged Glu-180 with uncharged Gln in the calf peptide did not
       significantly affect toxin binding, indicating Glu-180 alone does not
      comprise the anionic subsite on the receptor to which the cationic
      quaternary ammonium groups of cholinergic agents bind. d-Tubecurarine competed with texin binding to the modified call 30-may which lasks
       Glu-181 and Asp-190 present in Torpedu. Thus, the new subside obulible formed by another neg. charged residue or by 51 amino abiliside chain. It
       is possible that the post charges on cholinergic ligands are countered by a neg. electrostatic potential provided by polar groups, such as the
      hydroxyl group of tyrosine, present on several residues in this region, and the neg. charges present on any of residues 175, 167, 187, or 187. Equil. sath. binding or lalpha. Ebungary win to Torpe to peptige 186-284.
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revealed a minor bindiry component with an apparent FU of 4.0 mM and a major component with a KI or do mM. In the presence of 0.00 std, 1 binding component with a KI of 0.4 mM was detected. This compares with an

affinity of $KD \approx 0.41~\rm nM$ for towin binding to native adetylcholine receptor in the solid-phase assay. SDS may stabilize a conformation of

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the peptide that is conducive to high-affinity binding.

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ACCESSION NUMBER:
TITLE:
                              .alpha.=Tomin binding to adetyl tolline relegion .alpha.100=191 peptid=s: intrinsic fluoreseense
                              atudited
                             Radding, W.; Corfield, B. W. R.; Levinson, L. S.;
Hashim, G. A.; Low, B. W.
Howard Hughes Inst., Columbia Univ., New York, NY,
AUTHOB,J:
CORPORATE SOURCE:
                              10032, USĀ
SOURCE:
                              FEBS Letters (1988), 231(1), 212-16
                              CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE:
LANGUAGE:
                              Journal
                              English
      Interactions between 2 .alpha.-toxins and the synthetic peptides
      .alpha.179-191 from both calf and human abetylchilline receptor
      .alpha.-subunit sequences were studied by measurements of quenching of
     intrinsic fluorescence after toxin addn. Dissoon. consts. of .apprx.5
     .times. 10-8M for binding of calf peptide by both .alcha.-cobrotoxin and
     erabutowin a were estd. The binding of .alpha.-cobrotowin to calf
     peptide, which leads to marked quenching of flucrescence intensity, is
     inhibited by a 114M excess of abetyloholine. The human .alpha.179-191
     peptide binds to .alpha. -coprotomin, but not, under remparable conditions,
     to erabutoxin a.
     114753-46-7P
      RL: SPN (Synthetic preparation); PREP (Preparation)
         (prepn. of, of calf acetylcholine receptor .alpha.-subunits, and
         .alpha.-toxins binding by)
L15 ANSWER 17 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER:
                             1984:185956 HCAPLUS
DOCUMENT NUMBER:
TITLE:
                              100:195956
                             A super active cyclic hexapeptide analog of
                             sematestatin
AUTHOR(S):
                             Veber, Daniel F.; Saperstein, Richard; Nutt, Ruth F.;
                             Freidinger, Roger M.; Brady, Stephen F.; Curley, Paul;
                             Perlow, Debra S.; Paleveda, William J.; Colton, C.
                             Dylion; et al.
                             Merok Sharp and Dohme Res. 128., West Fount, EA,
CORPORATE SOURCE:
                             TP480, NUA
Life Shiences | 1 m4 , n4 14 , 1 m1 1 m
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SOURCE:
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                              Journal
LANGUAGE:
                             English
     Cyclo(N-methyl-Ala-Tyr-D-Trp-Lys-Val-Fhe) (I) [81377-02-8] was
AВ
     50-100-fold more potent than cyclic schatostatin [38916-34-6] for the inhibition of insulin [9004-10-8], glucagon [9007-90-5] and growth
     hormone [9002-71-6] release as revealed by structure-activity studies of cyclic hemapoptide analogs of schatostatic in rats. The hydroxyl group of
     tyrosine conterred a 10-fold enhancement to the potency. Fotency was also
     correlated with hydrophobicity. I improved the control of postprandial
     hyperglycemia in diabetic animals when given in combination with insulin. The analog was quite stable in the blood and in the gastrointestinal
     tract, but the bicavailability after oral administration was only 1-3-
     The biol. properties and long duration of I should allow clin. Abaluation
     of the inhibition of alucation release as an advict to instill in the
     treatrent of patients with diabetes.
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Table 3

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                                   170663-03-37BI OR 170663-04-47BI OR 170997-35-27BI OR 201529-09-
                                    1/BI OR 208192-30-7/BI OR 209487-88-6/BI OR 241814-61-7/BI OR
                                   301300-56-1/BI OR 432700-32-8/BI OR 434378-63-9/BI OR 89808-58-2
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L16 ANSWER 1 OF ME REGISTRY COPYRIGHT 2003 ACS
           434378-63-9 REGISTRY
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           L-Isoleucine, L-methionyl-L-seryl-L-tryptophyl-L-histidyl-L-seryl-L-
           tryptophyl-L-isoleucyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-.alpha.-glutamyl-
            L-isoleubyl-L-tyrosyl-L-leubyl-L-.alpha.-glutamyl-L-asparaginyl-L-threonyl-
             L-proly:-L-cysteiny:-L-tyrosy:-L-lysy:-L-tyrosy:-L-.alpha.-g::utamy:-L-
           threonyl-L-.alpha.-aspartyl-L-isoleucyl-L-leucyl-L-tyrosyl-L-isoleucyl-L-
           alanyl-1-seryl-1-phenylalanyl-1-.alpha.-aspartyl-1-phenylalanyl-1-seryl-1-
           arginyl-L-glutaminyl-L-isoleucyl-L-prolyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-seryl-L-threenyl-L-methionyl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl
           arginyl-1-isoleudyl-1-seryl-1-valyl-1-tyrdsyl-1-seryl-1-valyl- (901)
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           3444: PN: WGC19A5A3 SEQID: 844% claimed protein
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tystoinyl-L-, alpha, -aspartyl-L-leu ylqly yl-L-seryl-L-leu yl-L-dlutaminyl-
L-prolyl-L-prolyl-L-leucyl-L-prolyl-L-seryl-L-seryl-L-tryptophyl-L-, alpha, -
aspartyl-L-tyrosyl-L-arginyl-L-arginyl-L-, alpha, -glutamyl-L-soryl-L-leucyl-
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           valyl-L-prolyl-L-tryptuphyl-1-threcnyl-L-alanyl-1-try;fophyl-L-alanyl-1-
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           241814-51-7 REGISTRY
           L-Tyrosine, L-threenyl-L-valyl-L-seryl-L-arginyl-L-valyl-L-prolyl-L-
           tryptophyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-
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           208192-30-7 FERISTEY
           Slycine, L-alanyi-L-.alpha.-aspartylgiyoyl-L-alanyi-L-tryptophyl+L-
           pnenylalanyl-1-seryl-1-ryptophylalybyl-1-phenylalanyl-1-prolyl-1-
            glutaminyi-i-tryytighyi-i-tryktöxkylglycyi-i-alanyi-l-alahyi-1(901)
            ÎNDEK NAME;
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RN
           208192-30-7 REGISTRY
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          18
                    1 ADGAMESWGE POWMGAAG
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                      5-10
HITS AT:
REFERENCE 1: 129:91863
L16 AMSWER 7 OF 25 REGISTRY COPYRIGHT 2003 ACC
RN
          201529-09-1 REGISTRY
          L-Aspartic acid, L-tyrosyl-L-arginylglycyl-L-tryptcphyl-L-lysyl-L-histlidyl-
           LetryptophyleLevalyleLephenylalanyleLetyrosyleLethra hyleLebysteinyleLe
           cysteinyl-L-prolyl-L-.alpha.-aspartyl-L-threonyl-L-prolyl-L-tyrosyl-L-
           leucyl- (9CI) (CA INDEX NAME)
SQL
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                    1 YRGWKHWVFY TOOPDTEYLD
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HITS AT:
REFERENCE 1: 128:110913
L16 ANSWER 8 OF 25 REGISTRY COPYRIGHT 2003 ACS
          172997-35-2 REGISTRY
          L-Lysinamide, L-threonyl-L-tryptophyl-L-, alpha. -aspartyl-L-tryptophyl-L-phenylalanyl-L-seryl-L-tryptophyl-L-l-wobyl-L-phenylalanyl-L-seryl-L-tryptophyl-L-l-seryl- yl-1-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-seryl-L-sery
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F.11
     170663-04-4 REGISTRY
       l-Aspartic acid, L-.alpha.-glutamyi-l-alanyi-l-arqinylglycyl-l-tryptophyl-
      L-lysyl-l-histidyl-l-tryptophyl-l-valyl-l-phenylalanyl-l-tyrosyl-l-seryl-l-
pysteinyl-l-pysr-inyl-l-prolyl-l-threonyl-l-threonyl-l-histidyl-l-tyrosyl-
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              1: 103:37:217
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L16 AMSWER 10 OF 25 REGIMPRY CONTRINSION OF A MO
227
      170663-03-3 REGISTRY
      L-Aspartic acid, L-.alpha.-glutamyl-L-alamyl-L-arginylglycyl-L-tryptophyl-
      L-lysyl-L-histidyl-L-thyrtophyl-L-valyl-L-phenylaladyl-L-tyrosyl-i-sahyl-L-
pysteinyl-L-bysteinyl-L-soryl-L-threonyl-L-throonyl-L-prolyl-L-tyrosyl-L-
      leucyl- (9CI) (CA INDEX NAME)
RN
      170663-03-3 REGISTRY
      21
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           1 EARGWKHWYF YSCCSTTFYL D
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REFERENCE
            1: 123:330219
116 ANSWER 11 OF 28 REGISTRY COPYRIGHT / 13 Ans
      170663-02-2 REGISTRY
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      L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptcphyl-
      L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-
      oystelnyi-1-tryptophyl-1-prolýi-1-thrépnyl-1-threonyl-1-prolyl-1-tyrosýl-1-
leucyl- (901) (CA INDEX NAME)
      ledeyl- (987
SOL
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      170663-02-2 REGISTRY
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           l Eargwrhwuf Ysowfitfyl d
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HITS AT:
             5-10
            1: 123:330219
REFERENCE
116 AMSWER 12 OF 15 REGISTRY COPYRIGHT 1003 ACS
BN
      170663-01-1 REGISTRY
      L-Aspartic acid, L-.alpha.-qlutamyl-L-alanyl-L-arginylqlycyl-L-tryptophyl-
      L-lysyl-L-histidyl-L-tryphophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threcnyl-L-threcnyl-L-prolyl-L-tyrosyl-L-leucyl- (901) (0A INDEX NAME)
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      170663-01-1 REGISTRY
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HITS AT:
            1: 103:33:019
REFERENCE
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Die Amgwer 13 of 16 February in President Lose And
     170663-00-0 REGISTRY
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      L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylgly.yl-L-tryptiphyl-
      l-lysyl-L-histidyl-l-thyptophyl-l-valyl-l-phenylalanyl-L-tyr syl-l-alanyl-
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     170663-00-0 REGISTRY
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HITS AT:
REFERENCE 1: 123:330219
116 AMSWER 14 OF US REGISTRY COPYRIGHT 2003 AGS
     170662-99-4 REGISTRY
     L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-rryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrcsyl-L-alanyl-L-pysteinyl-L-cysteinyl-L-leucyl-L-threcnyl-L-threonyl-L-prolyl-L-tyrosyl-
     L+leucyl-1(901) (CA INDEX NAMÉ)
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L16 ANSWER 15 OF 25 REGISTRY COPYRIGHT 2003 ACS
F.N
     170662-98-3 REGISTRY
     L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-
      l-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-
     L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-
     tyrosyl-1-leucyl- (9CI) (CA INDEX NAME)
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     170662-98-3 REGISTRY
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REFERENCE 1: 123:330219
L16 ANSWER 16 OF 28 REGISTRY COFFRIGHT 2003 ACS
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     170662-94-9 REGISTRY
     L-Aspartic acid, L-.alpha.-dlutamyl-L-alanyl-l-ardinylglycyl-l-tryptophyl-
     Lelysyl-lehistidyl-letryktokhylelevalyl-lekhenylalanyleletyr syleleklanyle
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     170662-94-9 REGISTRY
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           157960-63-9 REGISTRY
           I-Tyrosine, Learginylylynyl-1-tryptophyl-1-lysyl-1-histidyl-1-tryptophyl-1-tryptophyl-1-tryptophyl-1-tryptophyl-1-tropyl-1-tryptophyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tropyl-1-tr
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            157960-63-9 REGISTRY
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REFERENCE
116 AMSWER 18 OF 28 REGISTRY CLEVELGHT 2018 ACC
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           155216-25-4 REGISTRY
           L-Alamine, L-threomyl-L-leubyl-L-methic myl-L-metyl-Letine my.-L-metyl-le
           alanyl-L-threonyl-L-alanyl-L-threonyl-L-lalpna.-Glumanyl-L-threonyl-L-
alanyl-j-threonyl-L-lysyl-L-anginyl-L-glumaninyl-L-lalpha.eglutanyl-L-
           threonyl-L-tryptophyl-L-,alpha.-aspartyl-L-tryptophyl-L-phenylalanyl-L-
           seryl-l-tryptophyl-l-leucyl-l-phenylalanyl-l-leucyl-l-prolyl-l-seryl-l-
           .alpha.-glutamyl-L-seryl-L-lysyl-L-asparaginyl-L-histidyl-L-leucyl-L-
           histidyl-1-threenyl-1-threenyl-1-threenyl-1-glutaminyl-1-methionyl- (901)
           (CA INDEX NAME)
OTHER NAMES:
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          Antigen CD 44 (human exen 6)
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           155216-25-4 REGISTRY
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                    1 TLMSTSATAT ETATKRQETW DWFSWLFLPS ESKNHLHTTT QMA
HITS AT:
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**RELATED SEQUENCES AVAILABLE WITH SEMIINE ..
REFERENCE 1: 10 :318415
L16 ANSWER 19 OF 25 REGISTRY COPYRIGHT 2003 ACS
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           133322-53-9 REGISTRY
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          133322-53-9 REGISTRY
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REFERENCE
                        1: 117:164626
                       11:4:21:21
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110
          133295-54-2 PEGISTRY
          l-Aspartin acid, l-sexpl-L-acginglylyd-l-tryptophyl-L-lysyl-L-histidyl-L-
          tryptophyl-l-valyl-l-phonylalanyl-l-lyb syl-l-lalabyl-l-systkinyl-l-
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                 114:223957
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    AMSWER 21 GE 25 REGISTRY CLEVELHET A 13 ACS
     133295-53-1 REGISTRY
     L-Serine, L-Lalpha.-glumamyl-L-serylglybyl-L-Lalpha.-glumamyl-L-mryptophyl-
      l-valyl-1-isoleudyl-1-lysyl-1-.alpha.-glutamyl-1-alanyl-1-arginylglydyl-1-
     tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-
     tyrosyl-[(93I)
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            13-18
REFERENCE
           1: 114:22385°
L16 ANSWER 22 OF 25 REGISTRY COPYRIGHT 2:13 ACS
RN
     115826-30-7 REGISTRY
CN
     L-Histidine, L-seryiglycyl-L-.alpha.-glutamyl-L-tryptophyl-L-valyl-L-
     methionyl-1-lysyl-1-lalpha.-glutamyl-1-seryl-1-arginylgljvyl-1-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-
     threonyl-L-cysteinyl+1-dysteinyl-1-prolyl-1-seryl-L-threonyl-1-prolyl-1-
     tyrosyl-L-leucyl-L-.alpha.-aspartyl-L-isoleucyl-L-threonyl-L-tyrosyl-
             (CA INDEX NAME)
     32
     115826-30-7 REGISTRY
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          1 SGEWYMKESR GWKHWVFYTC CRSTRYLDIT YH
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HITS AT:
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           1: 109:106149
    -ANSWER 23 OF 25 REGISTER CLEVELURT 1 13 ADS
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     115826-29-4 REGISTRY
     L-Histidine, L-Serylaly while alphanes of a world-ray repay elemany his isoleucy i-1-lysyl-L-shutaminy.-L-seryl-L-arsiny.shy wi-L-ray to pay i-L-lysyl-L-histidy i-L-tryptophyl-L-valyl-L-phenylalany i-L-tyrosyi-L-alany i-L-
     oysteinyl-1-cysteinyl-1-pholy(-1-sehyl-1-threonyl-1-prolyl-1-tyrosyl-1-
leucyl-1-lalpha.-aspartyl-1-isoleucyl-1-threonyl-1-tyrosyl- (901) (CA
     INDEX MAMES
     32
RN
     115826-29-4 BERISTRY
     32
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          1 SGEWULKÇAR GWAHAVEYAR OPSTEYLDIT YE
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116 AMSWER 24 OF 28 REGIOTRY CORPRESENT 1003 ACS
   114753-46-7 REGISTRY
    L-Alanine, L-lysyl-L-.alpha.-glutamyl-L-seryl-L-arginylglydyl-L-tryptophyl-
    \verb|l-lysyl-L-histidyl-L-nryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-|,s01||
   13
    114753-46-7 REGISTRY
    13
       1 KESROWKHWY FYA
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HITS AT:
REFERENCE 1: 113:128235
        109:2071
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116 AMSMER 25 OF 25 REGISTRY CORYRIGHT A UR AUS
   89808-58-2 REGISTRY
EN
    Cyclo(N-methyl-L-alanyl-2-icdo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-valyl-
    L-tryptophyl) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
   1,4,7,10,13,16-Hexaazacyclooctadecane, cyclic peptide deriv.

Cyclic(N-methyl-L-alanyl-2-iodo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-
    valyl=l=tryptophyl)
   ay alia
   modified
______
type ----- location ---- description
______
modification Ala-1 - methyl<Me>
modification Phe-2 - iod<<I>
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SQL 6
RN
   89808-58-2 REGISTRY
SQL 6
       1 AFWKVW
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HITS AT:
REFERENCE 1: 100:140/66
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